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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

:OM nucleic - nucleic search, using Bw model

Run on: January 31, 2004, 04:07:32 ; Search time 7213 Seconds
(without alignments) Million Cell-updates/sec

Title: US-10-017-085a-205
Sequence: 1 cgcctccggcttcgaggt.....aaaaaaaaaaaaaaa 1939

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues
Word size : 10

Total number of hits satisfying chosen parameters: 2792712
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : GenEmbl:
1: gb;ba:
2: gb;htg:
3: gb;in:
4: gb;om:
5: gb;ov:
6: gb;pat:
7: gb;Ph:
8: gb;pl:
9: gb;pr:
10: gb;ro:
11: gb;sts:
12: gb;sy:
13: gb;un:
14: gp;vi:
15: em;ba:
16: em;fun:
17: em;hum:
18: em;in:
19: em;mu:
20: em;om:
21: em;or:
22: em;ov:
23: em;pat:
24: em;ph:
25: em;pl:
26: em;ro:
27: em;sts:
28: em;un:
29: em;vi:
30: em;htg_hum:
31: em;htg_inv:
32: em;htg_other:
33: em;htg_mus:
34: em;htg_pln:
35: em;htg_rod:
36: em;htg_mam:
37: em;htg_vrt:
38: em;sy:
39: em;htg_hum:
40: em;htg_mus:
41: em;htg_other:

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1635	84.3	1964	9	BC015582	BC015582 Homo sapi
2	1497	77.2	1794	6	AK195174	AK195174 Sequence
3	1051	54.7	175020	9	AC024267	AC024267 Homo sapi
4	200	10.3	397	6	AK01778	AK01778 Sequence
5	52	2.7	103555	10	AL669840	AL669840 Mouse DNA
6	52	2.7	204628	2	AC048361	AC048361 Mus muscu
7	51	2.6	51	6	AK163165	AK163165 Sequence
8	42	2.4	245259	2	AC114124	AC114124 Rattus no
9	31	1.6	177877	2	AC133243	AC133243 Rattus no
10	27	1.4	413	4	AB054499	AB054499 Phrybeer.
11	27	1.4	561	11	GG3447	GG3447 SHGC-141356
12	27	1.4	616	8	LDAu3162	AJ003162 Laminaria
13	27	1.4	905	9	BC017773	BC017773 Homo sapi
14	27	1.4	917	10	BC022657	BC022657 Mus muscu
15	27	1.4	963	9	BC027481	BC027481 Homo sapi
16	27	1.4	1062	8	ASBARNASE	X96466_A Hispanica
17	27	1.4	1174	9	BC008472	BC008472 Homo sapi
18	27	1.4	1322	9	HSM00573	AL000072 Homo sapi
19	27	1.4	1433	9	HSU1813	U41813 Human Class
20	27	1.4	1433	11	GI19993	GI19993 SWSS700 Bri
21	27	1.4	1588	9	AK026173	AK026173 Homo sapi
22	27	1.4	1836	10	MUSM61	DI4849 Mus musculu
23	27	1.4	2061	9	BC000591	BC000591 Homo sapi
24	27	1.4	2363	10	BC052006	BC052006 Mus muscu
25	27	1.4	2793	3	AY05943	AY05943 Drosophil
26	27	1.4	2800	9	BC03596	BC03596 Homo sapi
27	27	1.4	5640	10	BC023754	BC023754 Mus muscu
28	27	1.4	35055	10	NCBI6114	AL151011 Neutospo
29	27	1.4	44496	10	AL645975	AL645975 Mouse DNA
30	27	1.4	61226	9	AL139392	AL139392 Human DNA
31	27	1.4	77448	2	AC069565	AC069565 Homo sapi
32	27	1.4	86064	8	AB013395	AB013395 Arabidops
33	27	1.4	111998	9	AC011509	AC011509 Homo sapi
34	27	1.4	114532	9	AC015950	AC015950 Homo sapi
35	27	1.4	114546	2	AC000382	AC000382 Homo sapi
36	27	1.4	129332	9	AL90028	AL90028 Human DNA
37	27	1.4	133797	2	AC05740	AC05740 Sub Scrot
38	27	1.4	141775	9	AC079949	AC079949 Homo sapi
39	27	1.4	149646	2	AL63536	AL63536 Homo sapi
40	27	1.4	158553	2	AC00937	AC00937 Homo sapi
41	27	1.4	158802	2	AC015589	AC015589 Homo sapi
42	27	1.4	159577	9	AC078955	AC078955 Homo sapi
43	27	1.4	164135	2	AC102228	AC102228 Mus muscu
44	27	1.4	166380	9	AC087237	AC087237 Homo sapi
45	27	1.4	166966	9	AC016970	AC016970 Homo sapi

ALIGNMENTS

RESULT 1
BC015582
LOCUS BC015582 1964 bp mRNA linear PRI 09-OCT-2001
DEFINITION Homo sapiens, clone MGC:23280 IMAGE:4637504, mRNA, complete cds.
ACCESSION BC015582
VERSION BC015582.1 GI:15990433
KEYWORDS MGC.
SOURCE
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1964)
AUTHORS Stratberg,R.
TITLR Direct Submission
JOURNAL Submitted (04-OCT-2001) National Institutes of Health, Mammalian
Pred. No. is the number of results predicted by chance to have a

QY	1691	CTTAAAGGACTCCCTTGGGTCTCACGTGAGTGAGGAGGAGGCTTGGATGACCAA	1750	Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Db	1542	CTTAAAGGACTCCCTTGGGTCTCACGTGAGTGAGGAGGAGGCTTGGATGACCAA	1601	Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Db	1751	GGGTCTGAGGCCAGGGCAGCTGGCTTAAAGTGGGTCTGAGAGTCAGGGGG	1810	Wiman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Db	1602	GGGTCTGAGGCCAGGGCAGCTGGCTTAAAGTGGGTCTGAGAGTCAGGGGG	1661	Direct Submission
Db	1721	CAGCTGGTATCGAGGAGCCCTGGAGTAGAAGGGAGCTTCAGGAGCTGGCT	1721	Submitted (20-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 120 Charles Street, Cambridge, MA 02141, USA
Oy	1871	GGGGTATCTGATCTGAGCCCTTGGATTAAGGGCTTACCGCC	1918	4 (bases 1 to 175020)
Db	1722	GGGGTATCTGATCTGAGCCCTTGGATTAAGGGCTTACCGCC	1769	Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Organism				Birren,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalek,B.,
DEFINITION		Homo sapiens chromosome 17, clone RP1-20B24, complete sequence.		Camara,J., Chang,J., Chazaro,B., Choeply,Y., Collymore,A.,
ACCESSION				Cook,A., Cooke,P., Dearellano,K., Devar,K., Diaz,J.S., Dodge,S.,
VERSION				Faro,S., Ferrer,P., Fitzgerald,M., Gage,D., Galagan,J.,
KEYWORDS				Gardyna,S., Gordo,S., Graham,L., Grand-Pierre,N., Hafez,N.,
SOURCE				Hagob,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
JOURNAL				Konat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,
REFERENCE				Lindblad-Tonk,K., Liu,G., MacLean,C., McDonald,P., Major,J.,
AUTHORS				Matthews,C., McCarthy,M., Meldrin,J., Menous,L., Minova,T.,
TITLE				Milena,V., Murphy,T., Nguyen,J., Nicol,R., North,C.,
JOURNAL		Homo sapiens (human)		Norman,C.H., O'Connor,T., O'Donnell,J., O'Neill,D., Oliver,J.,
REFERENCE				Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Ratta,R.,
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		Rise,C., Ropov,P., Roman,J., Roy,A., Schuaback,R.,
REFERENCE		Mammalia; Buteria; Primates; Catarrhini; Hominidae; Homo.		Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
AUTHORS	1	(bases 1 to 175020)		Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
TITLE		Birren,B., Nusbaum,C. and Lander,E.		Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
JOURNAL		Homo sapiens chromosome 17, clone RP1-20B24		Wiman,D., Young,G., Zainoun,J., Zemberk,L., Zimmer,A. and Zody,M.
REFERENCE	2	(bases 1 to 175020)		Direct Submission
AUTHORS		Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,		Submitted (17-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE		Bouck,A., Baldwin,J., Barna,N., Beck,P., Boguslavsky,L.,		On Jan 7, 2003 this sequence version replaced gi:24158556.
AUTHORS		Chopell,Y., Cojanglelo,M., Collins,S., Collymore,A., Cooke,P.,		All repeats were identified using RepeatMasker:
TITLE		DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M.,		Smith, A.P.A. & Green, P. (1996-1997)
JOURNAL		Fensterer,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,		http://ftp.genome.washington.edu/RM/RepeatMasker.html
REFERENCE		Galgan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,		-----
AUTHORS		Grand-Pierre,N., Grant,G., Hagob,B., Heaford,A., Horton,L.,		Center: Whitehead Institute/ MIT Center for Genome Research
TITLE		Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,		Center code: WIBR
JOURNAL		Klein,J., Lander,E., Largocq,E., Lashczky,J., Levine,R.,		Web site: http://www-sig.wi.mit.edu
REFERENCE		Lieu,C., Liu,G., Locke,P., MacDonald,P., Marquis,N., McCarthy,M.,		Contact: sequence_submissions@genome.wi.mit.edu
AUTHORS		McEwan,P., McGurk,A., McKernan,N., McSheeters,R., Meldim,J.,		-----
TITLE		Meneus,L., Minova,C., Miranda,C., Mleaga,V., Morrow,J., Naylor,J.,		Project Information
JOURNAL		Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M.,		Center Project name: L2111
REFERENCE		Peterson,K., Pierre,N., Pisani,C., Poilier,V., Raymond,C.,		Center clone name: 20_B_24
AUTHORS		Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,		-----
TITLE		Sevey,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,		Location/Qualifiers
JOURNAL		Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,		1. 175020
REFERENCE		Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,		/organism="Homo sapiens"
AUTHORS		Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and		/mot_type="genomic DNA"
TITLE		Zody,M.		/db_xref="taxon:9606"
JOURNAL		Direct Submission		/chromosome="17"
REFERENCE		Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		/map="17"
AUTHORS	3	(bases 1 to 175020)		/clone="RP1-20B24"
TITLE		Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,		/clone_lib="RPCI-11 Human Male BAC"
JOURNAL		Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukgalier,B.,		/complement(155..464)
REFERENCE		Camarata,J., Chang,J., Chazaro,B., Chopell,Y., Collymore,A.,		/rpt_family="AluSp"
AUTHORS		Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,		517..547
TITLE		Faro,S., Ferreira,P., Fit-Gerald,M., Gage,D., Galagan,J.,		/clone="RP1-20B24"
JOURNAL		Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hatzos,N.,		/rpt_family="RTTGN"
REFERENCE		Hagob,B., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C.,		complement(559..835)
AUTHORS		Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,		/rpt_family="AlusX"
TITLE		Lindblad-Tonk,K., Liu,G., MacLean,C., McDonald,P., Major,J.,		2222..2519
JOURNAL		Matthews,C., McCarthy,M., Meidrim,J., Meineus,L., Minova,T.,		/rpt_family="AlusX"
REFERENCE		Mlenqa,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C.,		2849..2976
AUTHORS		Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,		/rpt_family="AluJo"
TITLE		Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Repta,R.,		complement(3136..3439)
JOURNAL		Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R.,		/rpt_family="AlusX"
REFERENCE		Seaman,S., Severy,P., Smith,C., Spencer,B., Strange-Thomann,N.,		repeat_region
AUTHORS				/rpt_family="LIMCa"
TITLE				complement(6667..6993)
JOURNAL				/rpt_family="AluY"
REFERENCE				7077..7345
AUTHORS				/rpt_family="AluSx"
TITLE				repeat_region
JOURNAL				complement(7604..7645)

Query Match 54.7%; Score 1061; DB 9; Length 175020;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Index 0; Gaps 0;

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repeat_region	/rpt_family="AlusX"	complement(8364..8662)
repeat_region	8694..8831	/rpt_family="AluWb"
repeat_region	8832..9133	/rpt_family="AluY"
repeat_region	9143..9415	/rpt_family="AlusG"
repeat_region	10270..10579	/rpt_family="AlusQ"
repeat_region	10280..10574	/rpt_family="AlusX"
repeat_region	10575..10590	/rpt_family="(PA)n"
repeat_region	10591..10672	/rpt_family="(PA)n"
repeat_region	10873..10886	/rpt_family="AlusQ"
repeat_region	11232..11395	/rpt_family="FRAM"
repeat_region	11396..11711	/rpt_family="FRAM"
repeat_region	11712..11728	/rpt_family="Aluy"
repeat_region	12424..12558	/rpt_family="LIM4"
repeat_region	14827..15139	/rpt_family="AlusX"
repeat_region	15191..15223	/rpt_family="AluS"
repeat_region	15224..15467	/rpt_family="MIR"
repeat_region	15467..15781	/rpt_family="AlusQ"
repeat_region	15788..15981	/rpt_family="AluS"
repeat_region	15982..16040	/rpt_family="AlusC"
repeat_region	16056..16220	/rpt_family="LIMCa"
repeat_region	16330..16510	/rpt_family="L2"
repeat_region	16512..16745	/rpt_family="AluWb"
repeat_region	16746..17024	/rpt_family="L2"
repeat_region	17025..17325	/rpt_family="Aluy"
repeat_region	17326..17625	/rpt_family="AluW"
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unsafe	notes ">30 qual SNGL region"	complement(17531..17625)
unsafe	notes "<30 qual SNGL region"	complement(17549..17588)
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Matches 111; Conservative 0; Mismatches 1; Index 0; Gaps 0;

QY 807 CAGGGCTGTGACTGGAGCTTCTGCACATGTCCTCGATGCTGGCCACTTT 866
 Db 92043 CGGGCTGTGACTGGAGCTTCTGCACATGTCCTCGATGCTGGCCACTTT 91984
 QY 867 TCGGCCATTGGCTTGCTGCTGGCTGGCCACCAAGAGGGGGTGCAGACCCCTG 926
 Db 91983 TCGGCCATTGGCTTGCTGCTGGCTGGCCACCAAGAGGGGGTGCAGACCCCTG 91924
 QY 987 TCGAAAGGGTCAAGGGCATGAGCCCTAGGGAGATTTGCCACTGCGAT 1046
 Db 91863 TCGAAAGGGTCAAGGGCATGAGCCCTAGGGAGATTTGCCACTGCGAT 91804
 QY 1047 GCAAGGGCTGCAAGGGCTTGGCCCTGGGGAGATCTGAACCCGATGAGCCCTG 1106
 Db 91803 GCAAGGGCTGCAAGGGCTTGGCCCTGGGGAGATCTGAACCCGATGAGCCCTG 91864
 QY 1107 CTGAGGACTCAGGGGCCATTCAGACCCACCCCTGAGGGAGATCTGAACCCGAT 1166
 Db 91743 CTGAGGACTCAGGGGCCATTCAGACCCACCCCTGAGGGAGATCTGAACCCGAT 91684
 QY 1167 CTCACACTTACCCACCCCTGAGAGTCACCGAGATTGCTAGATGACGCCAATC 1226
 Db 91683 CTCACACTTACCCACCCCTGAGAGTCACCGAGATTGCTAGATGACGCCAATC 91624
 QY 1227 AGCTTAAGTTGAGCCATCCTCTTAACTCTCTAACCTCTAGGCCGAGTCCTGCGAT 1286
 Db 91623 AGCTTAAGTTGAGCCATCCTCTAACCTCTAACCTCTAGGCCGAGTCCTGCGAT 91564
 QY 1287 GCACTTATGGCTCTGAACCTCCAGTGTGAGATCCACTCTCTAACCTCTAGGCCGAGTCCTGCGAT 1346
 Db 91563 GCACTTATGGCTCTGAACCTCCAGTGTGAGATCCACTCTAACCTCTAGGCCGAGTCCTGCGAT 91504
 QY 1347 GTTGTGATCTGACCTCGGCGTTCTGGGCCCAAGCTGGCCCTGGAGCACTG 1406
 Db 91503 GTTGTGATCTGACCTCGGCGTTCTGGGCCCAAGCTGGCCCTGGAGCACTG 91444
 QY 1407 CTTTCCTGGTGAAGAAATATGGTGAATTTCCTCTGGAGACTGACAGTAACCCA 1466
 Db 91443 CTTTCCTGGTGAAGAAATATGGTGAATTTCCTCTGGAGACTGACAGTAACCCA 91384
 QY 1467 GATGGAGAGTAGGGTATGCTGAGCACTGCTCTGGAAATTGGATGTTGAGCT 1526
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 QY 1527 CAGGCCACCCATTGATCTGACAGCTCTGGAGAGGGAGTTGAGCT 1586
 Db 91323 CAGGCCACCCATTGATCTGACAGCTCTGGAGAGGGAGTTGAGCT 91264
 QY 1587 GATGCTCTGCCACATGGAGATTAGTGAATCTGACCTTCTGGAGCT 1646
 Db 91263 GATGCTCTGCCACATGGAGATTAGTGAATCTGACCTTCTGGAGCT 91204
 QY 1647 GTTAATTAACCCATTGAGCGGAATTAGCTCCCTTGCACCGCTAGCTGAAGTA 1706
 Db 91203 GTTAATTAACCCATTGAGCGGAATTAGCTCCCTTGCACCGCTAGCTGAAGTA 91144
 QY 1707 GGTCCTCACAGTGGAGAGGGCTGGAGCTGAGCTGAGCTGAGCT 1766
 Db 91143 GGTCCTCACAGTGGAGAGGGCTGGAGCTGAGCTGAGCTGAGCT 91084
 QY 1767 CGCACTGCCATGGAGGGCTGGAGCTGAGCTGAGCTGAGCTGAGCT 1826
 Db 91083 CGCACTGCCATGGAGGGCTGGAGCTGAGCTGAGCTGAGCTGAGCT 91024

TITLE	Direct Submission	Submitted (14-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL		
REFERENCE		
AUTHORS		
COMMENT	All repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	
TITLE		
JOURNAL		
FEATURES		
SOURCE		
3 (bases 1 to 204628)		1. 204628 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10990" /clone_lib="RCI-23 Female Mouse BAC" /notes="Assembly fragment clone_end_sp6 vector_side:left" 81213..9109 /note="assembly_fragment" 90210..02935 /note="assembly_fragment" 103016..11669 /note="assembly_fragment" 116770..131956 /note="assembly_fragment" 132057..148455 /note="assembly_fragment" 148556..200359 /note="assembly_fragment" 200460..204628 /note="assembly_fragment" clone_end:T7 vector_side:right" /note="assembly_fragment" clone_end:T7
BIRREN, B., Nusbaum, C., Lander, E., Abouelhail, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Batiest, V., Bloom, T., Boguslavsky, L., Bouthigater, B., Camarati, J., Chang, J., Cheepel, Y., Collimore, A., Cook, A., Cooke, B., Corum, B., Dearlano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, I., Brickton, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardna, S., Graham, L., Grand-Pierre, N., Hafez, N., Higoian, D., Higos, B., Hall, J., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keils, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihowa, T., Mleneti, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Rettar, R., Riese, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seainan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Teufay, S., Theodore, J., Topham, K., Travers, M., Vassilie, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, I., Zimmer, A., and Zody, M.		
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
On Mar 27, 2003 this sequence version replaced gi:8076973.		
DIRECT SUBMISSION		
JOURNAL		
COMMENT	All repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	
Center: Whitehead Institute / MIT Center for Genome Research		
Center code: WIBR		
Web site: http://www-seq.wi.mit.edu		
Contact: sequence submissions@genome.wi.mit.edu		
----- project Information		
Center project name: D7284		
Center clone name: 163_A_8		
----- Summary Statistics		
Sequencing vector: M13, M7815, 33% of reads		
Sequencing chemistry: plasmid, m13, 67% of reads		
Chemistry: dye-terminator		
Assembly program: Phrap, version 0.960731		
Consensus quality: 202765 bases at least Q40		
Consensus quality: 203217 bases at least Q30		
Consensus quality: 203451 bases at least Q20		
Insert size: 197000; agarose-fp		
Insert size: 201928; sum-of-contigs		
Quality coverage: 12.1 in Q20 bases; agarose-fp		
Quality coverage: 11.3 in Q20.		
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
1 81112..81122: contig of 100 bp		
1 81113..81122: gap of 100 bp		
1 81112..90109: contig of 8897 bp in length		
1 90110..90209: gap of 100 bp		

mbc_feature	/note="wgs-contig"	113391..114894
BASE COUNT	53423	/note="wgs-contig"
LOCUS	AC13243/c	133389
DEFINITION	Best Local Similarity 100%; Score 42; DB 2; Length 215259;	RESULT 9
VERSION	383	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KEYWORDS	ACCATGAGGTCACTTCATGGCTTCTAATGCCACTCTG 424	JOURNAL
SOURCE	1333948 RACATGAGGTCACTTCATGGCTTCTAATGCCACTCTG 133389	TITLE
ORGANISM	Rattus norvegicus	Unpublished
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	2 (bases 1 to 177877)	Rat Genome Sequencing Consortium.
REFERENCE	1 (bases 1 to 177877)	Direct Submission
AUTHORS	Muzny,D., Marie, Metzker,M., Lee, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,N., Anguiano,D., Anaya-bechini,V., Aoyagi,I., Ayrode,J.M., Faca,B., Baden,H., Baldwin,D., Bandaranaike,D., Babor,M., Barnsteed,M., Benahmed,F., Biswaloo,K., Blair,J., Blanckenburg,K., Blyth,P., Brown,M., Bryant,N., Buay,C., Burch,P., Burrell,K., Caldeon,E., Cardenas,V., Carter,K., Cavasos,I., Castrill,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Covis,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Dwyer-Carroll,L., De Andrade,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Duan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escott,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Fortin,L., Foster,M., Foster,P., Frazer,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Gaxza,M., Gubregtsis,B., Geer,K., Gil,I.R., Grady,M., Guerra,M., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,K., Hernandez,R., Hines,S., Hladun,S.L., Hodges,A., Hodges,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Islebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowalski,C., Kraft,C.M., Lebow,H., Levav,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Loreskuhiwa,L., Louiseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindarla,M., Mahmoud,M., Malloy,K., Margum,A., Margum,B., Manya,P., Martin,K., Martin,R., Martinez,B., Mawhinney,S., Mcleod,M., Mcneill,J., Meenen,E., Milovavilevic,A., Minar,G., Minia,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidas,M., Murphy,M., Nair,L., Nankervis,C., Norris,S., Newton,N., Nguyen,N., Norris,S., Nwakelueh,O., Okwonou,G., Olatunpamagboon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,P., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scheerer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sibson,I., Sitter,C.D., Smaje,D., Sned,A., Sodegren,E., Song,Y.-Z., Sorelle,R., Sobe,J., Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.H., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,P., Williams,G., Willson,R., Wiegert,R.,	Submitted (01-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	2 (bases 1 to 177877)	On Sep. 10, 2002 this sequence version replaced gi:22758715.
AUTHORS	Center project name: GDRJ	COMMENT
JOURNAL	Center clone name: CH230-10014	Genome Center
REFERENCE	3 (bases 1 to 177877)	Center code: BCM
AUTHORS	Web Site: http://www.hgsc.bcm.tmc.edu/	Project Information
JOURNAL	Contact: hgsc-hellobcm.tmc.edu/	Summary Statistics
REFERENCE	4 (bases 1 to 177877)	Sequencing Vector: Plasmid;
AUTHORS	Assembly: Dye-terminator Big Dye: 100% of reads	Chemistry:
JOURNAL	Assembly program: Phrap; version 0.990329	Dye-terminator
REFERENCE	5 (bases 1 to 177877)	Consensus quality: 120153 bases at least Q40
AUTHORS	Center project name: GDRJ	Consensus quality: 127137 bases at least Q30
JOURNAL	Center clone name: CH230-10014	Consensus quality: 132199 bases at least Q20
REFERENCE	6 (bases 1 to 177877)	-----
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JOURNAL	Center clone name: CH230-10014	-----
REFERENCE	7 (bases 1 to 177877)	-----
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JOURNAL	Center clone name: CH230-10014	-----
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REFERENCE	108 (bases 1 to 177877)</td	

		Best Local Similarity 100.0%; Pred. No. 3-5e-05; Mismatches 0; Indels 0; Gaps 0;					
Matches 31; Conservative							
QY	DB	1909 GTTCACG3CCAAAGAAAGAA 1939					
*	19008	contig of 1549 bp in length					
*	20557	gap of unknown length					
*	20657	contig of 1386 bp in length					
*	22042	gap of unknown length					
*	22143	contig of 1031 bp in length					
*	23174	gap of unknown length					
*	23274	contig of 1151 bp in length					
*	24224	contig of 1871 bp in length					
*	24425	gap of unknown length					
*	24525	contig of 1161 bp in length					
*	26395	gap of unknown length					
*	26496	contig of 1108 bp in length					
*	27656	gap of unknown length					
*	27757	contig of 1232 bp in length					
*	28988	gap of unknown length					
*	28989	contig of 1926 bp in length					
*	3089	contig of 2123 bp in length					
*	31014	gap of unknown length					
*	31115	contig of 2100 bp in length					
*	33215	gap of unknown length					
*	33315	contig of 2199 bp in length					
*	35514	gap of unknown length					
*	35614	contig of 2137 bp in length					
*	37742	gap of unknown length					
*	37843	contig of 1108 bp in length					
*	38950	gap of unknown length					
*	39051	contig of 1880 bp in length					
*	41723	gap of 2672 bp in length					
*	41823	contig of 2137 bp in length					
*	43959	gap of unknown length					
*	44059	gap of unknown length					
*	44060	contig of 3446 bp in length					
*	47505	gap of unknown length					
*	47606	contig of 2836 bp in length					
*	50442	gap of unknown length					
*	50541	contig of 3000 bp in length					
*	53342	gap of unknown length					
*	53642	contig of 2024 bp in length					
*	55666	gap of unknown length					
*	55766	contig of 1880 bp in length					
*	57745	gap of unknown length					
*	59802	contig of 1857 bp in length					
*	59603	gap of unknown length					
*	59702	gap of unknown length					
*	62147	contig of 2445 bp in length					
*	62148	gap of unknown length					
*	62248	contig of 2874 bp in length					
*	65122	gap of unknown length					
*	65221	contig of 3229 bp in length					
*	68850	gap of unknown length					
*	73113	contig of 4863 bp in length					
*	73514	gap of unknown length					
*	76579	contig of 3065 bp in length					
*	76679	gap of unknown length					
*	79296	contig of 2617 bp in length					
*	81954	gap of unknown length					
*	81955	contig of 2559 bp in length					
*	82055	gap of unknown length					
*	85114	contig of 2960 bp in length					
*	85115	gap of unknown length					
*	89089	contig of 3974 bp in length					
*	89188	gap of unknown length					
*	93408	contig of 4219 bp in length					
*	93508	gap of unknown length					
*	97240	contig of 3733 bp in length					
*	97340	gap of unknown length					
*	97341	contig of 5759 bp in length					
*	103100	gap of unknown length					
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*	106348	gap of unknown length					
*	106349	contig of 5935 bp in length					
*	112084	gap of unknown length					
*	112184	contig of 3412 bp in length					
*	115595	gap of unknown length					
*	115696	contig of 6613 bp in length					

		/codon_start=1 /product="triggering receptor expressed on myeloid cells" 1 /protein_id="AAH1773_1" /db_xref="GI:17389459" /translation="MVKTRWGLLMLAVELRATKTEPKVILKEGGQFLDVCDDY LEKFASSOKAWQITRDGEMPTTACERPERKSHVQGVHIDYDHGLRTRMVN LOVEGLYOCVYKOPPKPHEMLERIRLIVTKGSGTCSNESTONTYKIPPTK ALCPLVSPRTVQARPKSTADVPDSEINIINVDIRKRVPPVNIVILLAGPLSKS
BASE COUNT	258 a	224 c 224 g 199 t
ORIGIN		
Query Match	1.4%	Score 27; DB 9%; Length 905;
Best Local Similarity	100.0%	Pred. No. 0.0065; Mismatches 0; Indels 0; Gaps 0;
Matches	27;	Conservative
Qy	1913	ACCGCCAAAAMAAAAMAAAAMAAA 1939
Db	870	ACGCCCAAAAAMAAAAMAAA 896
RESULT 14		
LOCUS	BC022657	917 bp mRNA linear ROD 16-APR-2003
DEFINITION	Mus musculus hypothetical protein LOC225847, mRNA (cDNA clone IMAGE:4219507), partial cds.	
ACCESSION	BC022657	
VERSION	BC022657.1	GI:18490481
KEYWORDS		
SOURCE		Mus musculus (house mouse)
ORGANISM		
REFERENCE		Bukaytoya, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS		1 (bases 1 to 917) Stansberg, R.J., Feingold, B.A., Grouse, L.H., Derge, J.G., Klaunher, R.D., Collins, P.S., Wagner, L., Sheinman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bluetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Maruyama, K., Farmer, A.R., Rubin, G.M., Hong, L., Staphletton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udin, T., Toshiyuki, S., Abramson, R.D., Mulahy, S.J., Bosak, S.A., McLean, P.J., Malek, J.A., Gunaratne, P.H., Richard, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.N., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heaton, B., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A.C., Young, A.C., Shavchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grindulis, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kozlowski, M.I., Skalski, U., Smalius, D.E., Schenck, A., Schein, J.E., Jones, S.J., and Maza, M.A.
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16199-16903 (2002)	
MEDLINE	2238257	
PUBLISHED	12/4/7932	
REFERENCE	2 (bases 1 to 917)	
AUTHORS	Strausberg, R.	Direct Submission
TITLE		Submitted (01-EBB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.ncbi.nih.gov	Contact: MGC help desk Email: cgabbs@mail.nih.gov
COMMENT		Tissue Procurement: Jeffrey E. Green, M.D. DNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMN) Center, Stanford University School of Medicine, Stanford, CA 94305
BASE COUNT	231 a	255 c 247 g 184 t
ORIGIN		
Query Match	1.4%	Score 27; DB 10%; Length 917;
Best Local Similarity	100.0%	Pred. No. 0.0065; Mismatches 0; Indels 0; Gaps 0;
Matches	27;	Conservative
Qy	1913	ACCGCCAAAAMAAAAMAAAAMAAA 1939
Db	868	ACGCCCAAAAAMAAAAMAAA 894
RESULT 15		
LOCUS	BC027481	963 bp mRNA linear PRI 08-APR-2002
DEFINITION	Homo sapiens, clone IMAGE:5107160, mRNA, partial cds.	
ACCESSION	BC027481	
VERSION	BC027481.1	GI:20071959
KEYWORDS		
SOURCE		Homo sapiens (human)
ORGANISM		
REFERENCE		Bukaytoya, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Strausberg, R.	Direct Submission
TITLE		Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.ncbi.nih.gov	Contact: MGC help desk Email: cgabbs@mail.nih.gov
COMMENT		Tissue Procurement: ATCC DNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMN) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Run on: January 31, 2004, 04:39:02 ; Search time 126 Seconds
 (without alignments)
 6792.396 Million cell updates/sec

Title: US-10-017-085A-205
 Perfect score: 1939
 Sequence: 1 cgcctcggcttcggagct.....aaaaaaaaaaaaaaaaaaa 1939
 Scoring table: Oligo_NUC
 Gapop 60.0 , Gapext 60.0
 Searched: 569378 seqs, 220691566 residues

Word size : 10

Total number of hits satisfying chosen parameters: 239297

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Result No.	Score	Query Length	DB ID	Description
1	26	1.3	1525	3 US-09-157-003-4
2	26	1.3	1525	3 US-09-587-136-4
3	26	1.3	1525	4 US-08-927-165A-4
4	25	1.3	263	4 US-09-091-097-26
5	24	1.2	38	4 US-09-325-554-7
6	24	1.2	102	1 US-07-620-154A-10
7	24	1.2	102	2 US-08-097-554A-10
8	24	1.2	102	3 US-08-480-640A-10
9	24	1.2	102	3 US-08-295-802-10
10	24	1.2	102	3 US-08-686-968C-106
11	24	1.2	102	3 US-08-488-237A-10
12	24	1.2	102	4 US-08-375-692A-10
13	24	1.2	102	4 US-08-472-679H-10
14	24	1.2	102	PCT-US93-00324-10
15	24	1.2	108	1 US-07-820-154A-22
16	24	1.2	108	2 US-08-097-554A-32
17	24	1.2	108	3 US-08-480-640A-32
18	24	1.2	108	3 US-08-295-802-32
19	24	1.2	108	3 US-08-488-237A-32
20	24	1.2	108	4 US-08-375-692A-32
21	24	1.2	108	4 US-08-472-679H-32
22	24	1.2	108	PCT-US93-00324-32
23	24	1.2	111	2 US-08-097-554A-78
24	24	1.2	117	3 US-08-480-640A-78
25	24	1.2	117	3 US-08-295-802-78
26	24	1.2	117	3 US-08-486-968C-130
27	1.2	117	3 US-08-686-968C-144	

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 US-09-157-603-4
 Sequence 4, Application US/09157603
 Patent No. 6174694
 GENERAL INFORMATION:
 APPLICANT: Havre, Pamela A.
 APPLICANT: Rice, Michael C.
 APPLICANT: Holloman, William K.
 APPLICANT: Kmiec, Eric B.
 TITLE OF INVENTION: RBC2 Kinase
 FILE REFERENCE: 7991-034-999
 CURRENT APPLICATION NUMBER: US/09/157,603
 NUMBER OF SEQ ID NOS: 8
 SEQ ID NO 4
 LENGTH: 1525
 TYPE: DNA
 ORGANISM: Mus Musculus
 US-09-157-603-4
 Query Match 1.3%; Score 26; DB 3; Length 1525;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1914 CGCCCAAAACAAAAAAACAAAAAAA 1939
 Db 1459 CGGCCAAGAAAGAAAGAAAGAA 1484
 RESULT 2
 US-09-587-436-4
 Sequence 4, Application US/09587436
 Patent No. 6210916
 GENERAL INFORMATION:
 APPLICANT: Havre, Pamela A.
 APPLICANT: Rice, Michael C.
 APPLICANT: Holloman, William K.
 APPLICANT: Kmiec, Eric B.
 TITLE OF INVENTION: RBC2 Kinase
 FILE REFERENCE: 7991-034-999
 CURRENT APPLICATION NUMBER: US/09/587,436
 CURRENT FILING DATE: 2000-06-05
 PRIOR APPLICATION NUMBER: 09157,603
 PRIORITY APPLICATION NUMBER: 1998-09-21
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 1525
 TYPE: DNA

ALIGNMENTS

; ORGANISM: Mus Musculus
; US-09-587-436-4

; Query Match 1.3%; Score 26, DB 3, Length 1525;
; Best Local Similarity 100.0%, Pred. No. 0.05, Mismatches 0, Indels 0, Gaps 0;
; Matches 26, Conservative 0, MisMatches 0, Indels 0, Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: KMLEC, ERIC B.
; APPLICANT: RICE, MICHAEL C.
; APPLICANT: SMITH, SHERRY T.
; TITLE OF INVENTION: Mammalian and Human Rec2
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kimeragen, Inc.
; CITY: 300 Pheasant Run
; STATE: PA
; COUNTRY: USA
; ZIP: 18940

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,165A

; FILING DATE: 1998-06-04
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HANSBURG, DANIEL
; REGISTRATION NUMBER: 361565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-504-4444
; TELEFAX: 215-504-4545
; TELEX: 215-504-4444
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; STRANDEDNESS: double
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; US-08-927-165A-4

; RESULT 3

; Sequence 4, Application US/08927165A

; Patent No. 6410226

; GENERAL INFORMATION:

; APPLICANT: KIMMEL, WILLIAM K.

; APPLICANT: RICE, MICHAEL C.

; APPLICANT: SMITH, SHERRY T.

; TITLE OF INVENTION: Mammalian and Human Rec2

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP

; STREET: PO BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/091,097

; FILING DATE: 1998-06-04

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: WEINER, MARC S.

; REGISTRATION NUMBER: 32,181

; REFERENCE/DOCKET NUMBER: 1422-0346P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 263 base pairs

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; US-09-091-097-26

; Query Match 1.3%; Score 26, DB 4, Length 263;

; Best Local Similarity 100.0%, Pred. No. 0.05, Mismatches 0, Indels 0, Gaps 0;

; Matches 25, Conservative 0, MisMatches 0, Indels 0, Gaps 0;

; GENERAL INFORMATION:

; APPLICANT: WEIDEL, KURT

; APPLICANT: BRAND, JOACHIM

; TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX

; FILE REFERENCE: 024420-00008

; CURRENT APPLICATION NUMBER: US/09/325,554

; CURRENT FILING DATE: 1999-06-04

; PRIOR APPLICATION NUMBER: 198-24-900,4

; PRIOR FILING DATE: 1998-06-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patent-In version 3.1

; SEQ ID NO: 7

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; RESULT 4

; Sequence 26, Application US/09091097

; Patent No. 6432407

FEATURE: /FEATURE: misc.signal
 NAME/KEY: misc.signal
 LOCATION: (1). (1)
 OTHER INFORMATION: Phosphate linked to biotin via Aminolinker
 US-09-325-554-7

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 Best Local Similarity 100.0%; Pred. No. 0.52; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 US-07-820-154A-10/c
 Sequence 10. Application US/07820154A
 Patent No. 5382425

GENERAL INFORMATION:
 APPLICANT: Cochran, Ph.D., Mark D
 TITLER OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/820,154A
 FILING DATE: 19920113
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)977-9550
 TELEX: 422523

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base pairs
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CLONE: 520-17.5 (Junction B)

FEATURE:
 NAME/KEY: CDS
 LOCATION: 85..99
 OTHER INFORMATION: /codon_start= 85
 /function= "translational start of hybrid protein"
 OTHER INFORMATION: /product= "N-terminal peptide"
 OTHER INFORMATION: /number= 1
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA
 OTHER INFORMATION: sequence"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 100..102
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /partial

RESULT 7
 US-00-097-554A-10/c
 Sequence 10. Application US/08097554A
 Patent No. 5669312

GENERAL INFORMATION:
 APPLICANT: Cochran, Ph.D., Mark D
 TITLER OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 112

CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/097,554A
 FILING DATE: July 22, 1993
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)977-9550
 TELEX: 422523

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base pairs
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CLONE: 520-17.5 (Junction B)

FEATURE:
 NAME/KEY: CDS
 LOCATION: 85..99
 OTHER INFORMATION:
 OTHER INFORMATION: /codon_start= 85
 OTHER INFORMATION: "Translational start of hybrid protein"
 OTHER INFORMATION: /products= "N-terminal peptide"
 OTHER INFORMATION: /numbers= 1
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
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 FEATURE:
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 LOCATION: 100..102
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 OTHER INFORMATION: /codon_start= 100
 OTHER INFORMATION: /function= "marker enzyme"
 OTHER INFORMATION: /product= "Beta-Galactosidase"
 OTHER INFORMATION: /evidence= EXPERIMENTAL
 OTHER INFORMATION: /gene= "lacZ"
 OTHER INFORMATION: /number= 2
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
 PUBLICATION INFORMATION:
 AUTHORS: Ferrari, Franco A
 AUTHORS: Trach, Kathleen
 AUTHORS: Hoch, James A
 TITLE: Sequence Analysis of the spoOB Locus Reveals
 TITLE: a Polycistronic Transcription Unit
 JOURNAL: J. Bacteriol.
 VOLUME: 161
 ISSUE: 2
 PAGES: 556-562
 DATE: Feb.-1985
 US-08-097-554A-10

Query Match 1.2%; Score 24; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.47; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAGAAAGAAAGAAAGAAAGAA 1939
 Db 78 GCGCAAAAGAAAGAAAGAAAGAA 55

RESULT 8
 US-08-480-640A-10/C
 Sequence 10, Application US/08480640A
 ;
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 APPLICANT: Cochran, Mark D.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,640A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400

INFORMATION FOR SEQ ID NO: 10:
 SOURCE CHARACTERISTICS:
 LENGTH: 102 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CLONE: 520-17.5 (Junction B)

FEATURE:
 NAME/KEY: CDS
 LOCATION: 85..99
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /codon_start= 85
 OTHER INFORMATION: "Translational start of hybrid protein"
 OTHER INFORMATION: /functions= "N-terminal peptide"
 OTHER INFORMATION: /product= "Beta-Galactosidase"
 OTHER INFORMATION: /numbers= 1
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
 OTHER INFORMATION: /sequence= "Translation of synthetic DNA sequence"
 PUBLICATION INFORMATION:
 AUTHORS: Ferrari, Franco A
 AUTHORS: Trach, Kathleen
 AUTHORS: Hoch, James A
 TITLE: Sequence Analysis of the spoOB Locus Reveals
 TITLE: a Polycistronic Transcription Unit
 JOURNAL: J. Bacteriol.
 VOLUME: 161
 ISSUE: 2
 PAGES: 556-562
 DATE: Feb.-1985
 US-08-480-640A-10

Query Match 1.2%; Score 24; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.47; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAGAAAGAAAGAAAGAAAGAA 1939
 Db 78 GCGCAAAAGAAAGAAAGAAAGAA 55

RESULT 9
 US-08-295-802-10/C
 Sequence 10, Application US/08295802
 ;
 GENERAL INFORMATION:
 APPLICANT: Cochran Ph.D., Mark D
 APPLICANT: Cochran Ph.D., Mark D
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 188
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/295, 802

FILING DATE: Herewith

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: 422523

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 base pairs

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Plasmid

IMMEDIATE SOURCE:

CLONE: 520-17.5 (Junction B)

FEATURE:

NAME/KEY: CDS

LOCATION: 85..99

OTHER INFORMATION: /codon_start= 85;

/function= "Translational start of hybrid protein"

/product= "N-terminal peptide"

/numbers= 1

/standard_name= "Translation of synthetic DNA

/other_information: sequence

FEATURES:

NAME/KEY: CDS

LOCATION: 100..102

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /partial

OTHER INFORMATION: /codon_start= 100

OTHER INFORMATION: /functions= "marker enzyme"

/products= "Beta-Galactosidase"

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /genes= "lacZ"

OTHER INFORMATION: /numbers= 2

OTHER INFORMATION: /citation= ([1])

PUBLICATION INFORMATION:

AUTHORS: Ferari, Franco A

AUTHORS: Trach, Kathleen

AUTHORS: Hoch, James A

TITLE: Sequence Analysis of the spoB Locus Reveals

TITLE: a Polycistronic Transcription Unit

JOURNAL: J. Bacteriol.

VOLUME: 161

ISSUE: 2

PAGES: 556-562

DATES: Feb, 1995

US-08-295-802-10

Query Match

Best Local Similarity

Matches

QY

1916

GCCAAAGAAAGAAAGAAAGAA 1939

Db

78

GCCAAAGAAAGAAAGAAAGAA 55

RESULT: 11

US-08-488-237A-10/C

Sequence 10, Application US/08488237A

Patent No. 621351

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: Recombinant Swinepox Virus

FILE REFERENCE: 39119-H/JML

CURRENT APPLICATION NUMBER: US/08/686, 968C

CURRENT FILING DATE: 1996-07-25

NUMBER OF SEQ ID NOS: 231

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 106

LENGTH: 102

TYPE: DNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence

OTHER INFORMATION: vector 520-17.5

US-08-686,968C-106

Query Match 1.2%; Score 24; DB 3; Length 102;

Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov 1916 GCCAAAGAAAGAAAGAAAGAA 1939

Db 78 GCCAAAGAAAGAAAGAAAGAA 55

RESULT: 11

US-08-488-237A-10/C

Sequence 10, Application US/08488237A

Patent No. 6213403

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488, 237A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-6400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Plasmid

IMMEDIATE SOURCE:

CLONE: 520-17.5 (Junction B)

RESULT: 10

US-08-686-968C-106/c

FEATURE: CDS
NAME/KEY: CDS
LOCATION: 85..99
OTHER INFORMATION: /codon_start= 85
OTHER INFORMATION: /function= "Translational start of hybrid protein"
OTHER INFORMATION: /product= "N-terminal peptide"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 100..102
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /codon_start= 100
OTHER INFORMATION: /functions "marker enzyme"
OTHER INFORMATION: /product= "Beta-Galactosidase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "lacZ"
PUBLICATION INFORMATION:
AUTHORS: Ferrari, Franco A
AUTHORS: Trach, Kathleen
AUTHORS: Hoch, James A
TITLE: Sequence Analysis of the spoB Locus Reveals
JOURNAL: J. Bacteriol.
VOLUME: 161
ISSUE: 2
PAGES: 556-562
DATE: Feb.-1985
LT 12
8-375-992A-10/C
Query Match 1.2%; Score 24; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;
SEQUENCE 10, Application US/08375992A
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David B.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 220.
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,992A
FILING DATE: Herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400

FEATURE: CDS
NAME/KEY: CDS
LOCATION: 85..99
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
NAME/KEY: CDS
CLONE: 520-17.5 (junction B)
FEATURE:
NAME/KEY: CDS
LOCATION: 85..99
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OTHER INFORMATION: /function= "Translational start of hybrid protein"
OTHER INFORMATION: /product= "N-terminal peptide"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
FEATURE:
NAME/KEY: CDS
LOCATION: 100..102
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /codon_start= 100
OTHER INFORMATION: /functions "marker enzyme"
OTHER INFORMATION: /product= "Beta-Galactosidase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "lacZ"
PUBLICATION INFORMATION:
AUTHORS: Ferrari, Franco A
AUTHORS: Trach, Kathleen
AUTHORS: Hoch, James A
TITLE: Sequence Analysis of the spoB Locus Reveals
JOURNAL: J. Bacteriol.
VOLUME: 161
ISSUE: 2
PAGES: 556-562
DATE: Feb.-1985
US-08-375-992A-10
Query Match 1.2%; Score 24; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SEQUENCE 10, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salfeld
STREET: 2000 Gilloping Hill Road
CITY: Kenvorth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #11.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmid
IMMEDIATE SOURCE:
CLONE: 520-17.5 (Junction B)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..102
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial/codon_start= 100
/functions= "marker enzyme"/products= "Beta-Galactosidase"
/evidences= EXPERIMENTAL
/genes= "lacZ"
/number= 2
/citations= {[1]}
PUBLICATION INFORMATION:
AUTHORS: Ferrari, Franco A; Trach, Kathleen; Hoch, James A
TITLE: Sequence Analysis of the spoOB Locus Reveals a
Patent No. 6497882
Polycistrionic Transcription Unit
JOURNAL: J. Bacteriol.
VOLUME: 161
ISSUE: 2
PAGES: 556-562
DATE: Feb. 1985
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-472-679H-10

Query Match 1 Best Local Similarity 1.2%; Score 24; DB 4; Length 102;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAMAAAAMAAAAMAAA 1939
Db 78 GCCAAAMAAAAMAAAAMAAA 55

RESULT 14
PCT-US93-00324-10/C
Sequence 10, Application PC/rus9300324
GENERAL INFORMATION
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E

TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #11.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00324
FILING DATE: 19930113
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: NUCLEAR ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmid
IMMEDIATE SOURCE:
CLONE: 520-17.5 (Junction B)

FEATURE:
NAME/KEY: CDS
LOCATION: 85..99
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 85/functions= "Translational start of hybrid protein"
/functions= "marker enzyme"/products= "Beta-Galactosidase"
/evidences= EXPERIMENTAL
/genes= "lacZ"
/number= 2
/citations= {[1]}

PUBLICATION INFORMATION:
AUTHORS: Ferrari, Franco A; Trach, Kathleen; Hoch, James A
TITLE: Sequence Analysis of the spoOB Locus Reveals a
Patent No. 6497882
Polycistrionic Transcription Unit
JOURNAL: J. Bacteriol.
VOLUME: 161
ISSUE: 2
PAGES: 556-562
DATE: Feb. 1985
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-472-679H-10

Query Match 1 Best Local Similarity 1.2%; Score 24; DB 4; Length 102;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAMAAAAMAAAAMAAA 1939
Db 78 GCCAAAMAAAAMAAAAMAAA 55

RESULT 14
PCT-US93-00324-10/C
Sequence 10, Application PC/rus9300324
GENERAL INFORMATION
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E

TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #11.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00324
FILING DATE: 19930113
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: NUCLEAR ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmid
IMMEDIATE SOURCE:
CLONE: 520-17.5 (Junction B)

FEATURE:
NAME/KEY: CDS
LOCATION: 85..99
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 85/functions= "Translational start of hybrid protein"
/functions= "marker enzyme"/products= "N-terminal peptide"
/evidences= EXPERIMENTAL
/genes= "lacZ"
/number= 2
/citations= {[1]}

PUBLICATION INFORMATION:
AUTHORS: Ferrari, Franco A; Trach, Kathleen; Hoch, James A
TITLE: Sequence Analysis of the spoOB Locus Reveals a
Patent No. 6497882
Polycistrionic Transcription Unit
JOURNAL: J. Bacteriol.
VOLUME: 161
ISSUE: 2
PAGES: 556-562
DATE: Feb. 1985
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-472-679H-10

Query Match 1 Best Local Similarity 1.2%; Score 24; DB 5; Length 102;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAMAAAAMAAAAMAAA 1939
Db 78 GCCAAAMAAAAMAAAAMAAA 55

RESULT 14
PCT-US93-00324-10/C
Sequence 10, Application PC/rus9300324
GENERAL INFORMATION
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY -1916 GCCAAGAAAGAAAGAAAGAAA 1939

Db 78 GCCAAGAAAGAAAGAAAGAAA 55

RESULT 15

US-07-820-154A-32/C

; Sequence 32, Application US/07820154A

Patent No. 538225

GENERAL INFORMATION:

APPLICANT: Cochran Ph.D., Mark D.

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEES: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

Country: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/820,154A

FILING DATE: 19920113

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)977-9550

TELEFAX: (212)664-0525

TELEX: 422223

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 base pairs

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Plasmid

IMMEDIATE SOURCE:

FEATURE: 538-46.26 (Junction B)

FEATURE:

NAME/KEY: exon

LOCATION: 88..102

OTHER INFORMATION: /codon_start= 88

OTHER INFORMATION: /function= "Translational start of hybrid protein"

OTHER INFORMATION: /product= "N-terminal peptide"

OTHER INFORMATION: /number= 1

OTHER INFORMATION: /standard_name= "Translation of synthetic DNA

OTHER INFORMATION: /sequence= "Translation of synthetic DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 103..108

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /partial

OTHER INFORMATION: /codon_start= 103

OTHER INFORMATION: /product= "NDV Hemagglutinin-Neuraminidase"

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /genes= "HN"

OTHER INFORMATION: /number= 2

Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;

QY -1916 GCCAAGAAAGAAAGAAA 1939

Db 81 GCCAAGAAAGAAAGAAA 59

Search completed: January 31, 2004, 08:03:22
Job time : 128 secs

Query Match 1.2%; Score 24; DB 1; Length 108;

PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0077339.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079563.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 29-APR-1998; 98US-0083352.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 30-APR-1998; 98US-0083559.
 PR 05-MAY-1998; 98US-0083742.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084641.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.

PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087398.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094551.
 PR 11-SEP-1998; 98US-0100038.
 XX (GETH) GENENTECH INC.
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 DR WPI; 1999-55138/46.
 P-PSDB; AAV41715.

XX New Secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -

XX Claim 2; Fig 74; 530pp; English.

The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ3381 to AAZ3438, and AAIV1685 to AAIV4174 represent Polynucleotide and polypeptide sequence given in the exemplification of the present invention.

XX Sequence 1939 BP; 367 A; 549 C; 624 G; 399 T; 0 other;

Query Match 100.0%; score 1939; DB 20; Length 1939; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Conservative 0; Indels 0; Gaps 0; Matches 1939;

QY	1 CGCTCTCCCTGGAGCTAAGGCGCCGCGCGCGCTTCAGGCCCTGTGAGGGCAT	60
Db	1 CGCTCTCCCTGGAGCTAAGGCGCCGCGCGCGCTTCAGGCCCTGTGAGGGCAT	60
QY	61 CGCAGGCCTGGCGATCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	120
Db	61 CGCAGGCCTGGCGATCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	120
QY	121 CGCGGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	180
Db	121 CGCGGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	180
QY	181 CTACTAACCTGGTGAAGGCCCGCGCTGGGGGGGGGGGGGGGGGGGGGGGG	240
Db	181 CTACTAACCTGGTGAAGGCCCGCGCTGGGGGGGGGGGGGGGGGGGGGG	240
QY	241 GCGCGTGTCAAGGCCAACAGGGCATCGGAAAGTGACGGCTGGGGGGGG	300
Db	241 GCGCGTGTCAAGGCCAACAGGGCATCGGAAAGTGACGGCTGGGGGGGG	300
QY	301 CGCGGAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	360
Db	301 CGCGGAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	360
QY	361 CGACCTCCGAGAGGTGGGACATGAGTCATTCATGGCTTGACTTGCCAG	420
Db	361 CGACCTCCGAGAGGTGGGACATGAGTCATTCATGGCTTGACTTGCCAG	420
QY	421 TCTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	480
Db	421 TCTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	480
QY	481 CCTCATCACAGTGGGGTATGTTCTGGGGGGGGGGGGGGGGGGGGGG	540
Db	481 CCTCATCACAGTGGGGTATGTTCTGGGGGGGGGGGGGGGGGGGGGG	540

QY 541 GCTTCGGTGGACCATATGCGTCCCTCTCTGTACACATGCTGCTGCTGACTGCTTCCTGAA 600
 Db 541 GTTCTGGTGGACCATATGCGTCCCTCTCTGTACACATGCTGCTGCTGACTGCTTCCTGAA 600
 QY 601 GGCATCTGCCCTAGCGCGGGTGTTGGTGTGCTCACCTGCCACTGTCGGGAGCT 660
 Db 601 GGCATCTGCCCTAGCGCGGGTGTTGGTGTGCTCACCTGCCACTGTCGGGAGCT 660
 QY 661 TCACTCAAAACCCCTGGACGCCCAAGGGCTGGTGGCTGGCTGGCGGAGACTGGGGCATATGC 720
 Db 661 TCACTCAAAACCCCTGGACGCCCAAGGGCTGGTGGCTGGCTGGCGGAGACTGGGGCATATGC 720
 QY 721 TGACACTAAGCTGGCTATGACTGTGCTGGGGAGCTGCCAACAGGTTGGCCAC 780
 Db 721 TGACACTAAGCTGGCTATGACTGTGCTGGGGAGCTGCCAACAGGTTGGCCAC 780
 QY 781 TGGCCTGACCTCTANGGACCCACCTGGTGGCTGGAGGACTGGGATATGGGATATGC 720
 Db 781 TGGCCTGACCTCTANGGACCCACCTGGTGGCTGGAGGACTGGGATATGGGATATGC 720
 QY 841 TETTCCTGGTAGCTGCTATGAGCCACCAGGGCTGGCTGGAGGACTGTCTGGGCA 840
 Db 841 TETTCCTGGTAGCTGCTATGAGCCACCAGGGCTGGCTGGAGGACTGTCTGGGCA 840
 Db 841 TETTCCTGGTAGCTGCTGGCCACTTGGGCCATGGCTGGGAGCTGGGATATGGGATATGC 900
 QY 901 AAGAGGGGGTCCCAGAACCCCTGTTGCTCACAGAGGCTATGGCCCTTAG 960
 Db 901 AAGAGGGGGTCCCAGAACCCCTGTTGCTCACAGAGGCTATGGCCCTTAG 960
 QY 961 TGGGAGATATTGCGCACTGCTGCTCACAGGGCTGGCCCTTAG 1020
 Db 961 TGGGAGATATTGCGCACTGCTGCTCACAGGGCTGGCCCTTAG 1020
 QY 1021 GCGAGCCATCGCTATGGAGGGCCAGCAGGGCTGGCCCTGGGAGGA 1080
 Db 1021 GCGAGCCATCGCTATGGAGGGCCAGCAGGGCTGGCCCTGGGAGGA 1080
 QY 1081 TCTCTGAACCGTGAAGACCCAGCTGAGACTCTGAGGGCTGGCCCTGGGAGGA 1140
 Db 1081 TCTCTGAACCGTGAAGACCCAGCTGAGACTCTGAGGGCTGGCCCTGGGAGGA 1140
 QY 1141 CCCAACCTCTGGAGGCCAACCTGGCTGGCCCTGGGAGGA 1200
 Db 1141 CCCAACCTCTGGAGGCCAACCTGGCTGGCCCTGGGAGGA 1200
 QY 1201 TTGTCTAAGATGACGCCAACCTGGCTGGCCCTGGGAGGA 1260
 Db 1201 TTGTCTAAGATGACGCCAACCTGGCTGGCCCTGGGAGGA 1260
 QY 1261 ACCTCTGGCCAGGAGCTTCCATGCTCATGTCCTGAAACCTGGGAGTGTTG 1320
 Db 1261 ACCTCTGGCCAGGAGCTTCCATGCTCATGTCCTGAAACCTGGGAGTGTTG 1320
 QY 1321 TGGGGCATGGCTGCACTGACCTGACGGTTTGATCTGGCTGGTACTTTCTGG 1380
 Db 1321 TGGGGCATGGCTGCACTGACCTGACGGTTTGATCTGGCTGGTACTTTCTGG 1380
 QY 1381 GCCCCAAGCTGCGCTGACATCTTCTGGTGAAGATAATGGGGTATT 1440
 Db 1381 GCCCCAAGCTGCGCTGACATCTTCTGGTGAAGATAATGGGGTATT 1440
 QY 1441 TCTTCCTGAGAGTGTGACAGTAAACCCAGATGGAGAGTACCGGTGCTGCTGCTG 1500
 Db 1441 TCTTCCTGAGAGTGTGACAGTAAACCCAGATGGAGAGTACCGGTGCTGCTGCTG 1500
 QY 1501 TCTCGGAAATTGGAGTGTGACAGTAAACCCAGATGGAGAGTACCGGTGCTGCTG 1560
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 QY 1561 GAGCAGAGGAGGGAGTTGCGATGATGACTGCAACTGAGAATTTGACTGA 1620
 Db 1561 GAGCAGAGGAGGGAGTTGCGATGATGACTGCAACTGAGAATTTGACTGA 1620

RESULT 2
 AAX87266 ID AAX87266 standard; cDNA, 1939 BP.
 XX AC AAX87266;
 XX DT 27-SEP-1999 (first entry)
 XX DB CDNA clone encoding human PRO853, amplified in tumour cells.
 XX KW PRO853; UNQ415; tumour; cancer; diagnosis; therapy; human; ds.
 XX OS Homo sapiens.
 XX PH
 FT CDS
 FT
 FT sig_peptide /tag=a
 FT mat_Peptide /tag=b
 FT /tag=c
 XX PN W09935170-A2.
 XX PD 15-JUL-1999.
 XX PP 05-JAN-1999; 99WO-US00106.
 XX PR 20-NOV-1998; 98US-010304.
 PR 05-JUN-1998; 98US-0070440.
 PR 29-DR-1998; 98US-003500.
 PR 22-MAY-1998; 98US-0086414.
 PR 10-JUN-1998; 98US-0086742.
 PR 10-NOV-1998; 98US-0107783.
 XX PA (GETH) GENENTECH INC.
 XX PI Botttein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 PI Roy MA, Wood WI;
 XX DR WPI; 1999-430185/35.
 DR P-PSDB; AAY06489.

Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment
 Example 1; FIG 25A-B; 162pp; English.

This is the nucleotide sequence of cDNA clone DNA48227 (ATCC 209812) coding for human PRO853 (TNO419) (see AAY06419). The clone was isolated from a human foetal kidney tissue library. Amplification of DNA48227 (chromosome 17) occurs in various tumours, especially colon tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed to PRO853 may have use in cancer therapy. The invention identifies 14 genes (see AAXB1254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment.

Db 781 TGGCGTACCTGCTTGAGGCCAACCCAGGCCATGAGGCCATGGCC 840
 QY 841 TGTCTCTGAGTGGCGCCACTTTGCCCCATTGGCTTGCTGCTGCTCAG 900
 Db 841 TGTCCTGGATGGCTGCCACTTTGCCCATGGCTGGCTGCTGCTCAG 900
 QY 961 TGGGAAATTGCGCACTGCGATGGAGAGGTGCCTCAGGCG 1020
 Db 961 TGGAGAATTTGCGCACTGCGATGGAGAGGTGCCTCAGGCG 1020
 QY 1021 GGCAGGCCATGGCTAGGAGGGCG 1080
 Db 1021 GGCAGGCCATGGCTAGGAGGGCG 1080
 QY 1081 TCGTGAACCGATGAGAACCCAGCTGAGGACTCAGAGGCCATCTCTAGAC 1140
 Db 1081 TCGTGAACCGATGAGAACCCAGCTGAGGACTCAGAGGCCATCTCTAGAC 1140
 QY 1141 CCCCAACCTGAGGAGGCCAGTTCTCACTTAACCCAGCCCTAGCTCACAGA 1200
 Db 1141 CCCCAACCTGAGGAGGCCAGTTCTCACTTAACCCAGCCCTAGCTCACAGA 1200
 QY 1201 TTGTTGTAATGACCGAACCGAACTTCAGSCTAAGTCTGACCTTGAGCTCTTA 1260
 Db 1201 TTGTTGTAATGACCGAACCGAACTTCAGSCTAAGTCTGAGGAGCCATCTCTAGAC 1260
 QY 1261 ACCCTAGGGAGGAGCTCTGCTGACTCTGAGCTTCTGAACTGGATGGCTCAGA 1320
 Db 1261 ACCCTAGGGAGGAGCTCTGCTGACTCTGAGCTTCTGAACTGGATGGCTCAGA 1320
 QY 1321 TGAGGCATGCCATGACACTGACGGTTAGGCTAACCTGAGCTGCTG 1380
 Db 1321 TGAGGCATGCCATGACACTGACGGTTAGGCTAACCTGAGCTGCTG 1380
 QY 1381 GCCCCAAGCTGCCATGACACTCTCTCTCTGAGGATAATGGTATT 1440
 Db 1381 GCCCCAAGCTGCCATGACACTCTCTCTGAGGATAATGGTATT 1440
 QY 1441 TCTCTTGAGGTGAGTAAACCCGATGGAGAGTAGGGTCTCTAGACACTGGCT 1500
 Db 1441 TCTCTTGAGGTGAGTAAACCCGATGGAGAGTAGGGTCTCTAGACACTGGCT 1500
 QY 1501 TCTCGAAATTGGTAGGTTAGGCCCCACCTTATGATCTGATCACCTCTG 1560
 Db 1501 TCTCGAAATTGGTAGGTTAGGCCCCACCTTATGATCTGATCACCTCTG 1560
 QY 1561 GAGCAGGGAGGGAGTTGCAATGATGAGTAGGCTAACCCGATGGCTGCTG 1620
 Db 1561 GAGCAGGGAGGGAGTTGCAATGATGAGTAGGCTAACCCGATGGCTGCTG 1620
 QY 1621 TCCCTTGACCGGTAGTTGAGTAAATCCCCATGTTATGAGGCCATTA 1680
 Db 1621 TCCCTTGACCGGTAGTTGAGTAAATCCCCATGTTATGAGGCCATTA 1680
 QY 1681 GCTCCCGAGGTAAGGAGCTGCCATGGGCTCACTGAGGAGGCCCTGGAT 1740
 Db 1681 GCTCCCGAGGTAAGGAGCTGCCATGGGCTCACTGAGGAGGCCCTGGAT 1740
 QY 1741 CTGACCCAAAGGTCTGAGGCCAGGGCGACTGCGCTGAGTGGCTGGAGT 1800
 Db 1741 CTGACCCAAAGGTCTGAGGCCAGGGCGACTGCGCTGAGTGGCTGGAGT 1800
 QY 1801 CAGGGAGGGAGGTGAGTGGCTGAGGCCATGGGCTCACTGAGGAGGCC 1860
 Db 1801 CAGGGAGGGAGGTGAGTGGCTGAGGCCATGGGCTCACTGAGGAGGCC 1860
 QY 1861 ATGCGAGGCTGGGATCTGATCTGAGGCCCTGGATAAACCGCGTGAACGCCAA 1920

QY	1081	TGGTAACTCCGATGAGAACCCAGTCAGGACTCAGNGCCCACCTCTCTAGCAC	1020
QY	1021	GGCAAGCCCATCGCTATGGAGGCCAGAGGCCTCGAGGCTTGAGGCTGGGAGGA	1080
Db	1021	GGCAAGCCCATCGCTATGGAGGCCAGAGGCCTCGAGGCTTGAGGCTGGGAGGA	1080
QY	1141	CCCCACCTGAGGAGCCACAGTTCTCACCTTACCCAGCCCTAGAGTCACCGA	1200
Db	1141	CCCCACCTGAGGAGCCACAGTTCTCACCTTACCCAGCCCTAGAGTCACCGA	1200
QY	1201	TTRGCTTAGATGAGCAGCAGGATTAGCTTAAGTGAGCTGAGATCCAGCTCA	1260
Db	1201	TTRGCTTAGATGAGCAGCAGGATTAGCTTAAGTGAGCTGAGATCCAGCTCA	1260
QY	1261	ACCTCAGCCAGGATCTGGCACTCTGGTCTTGAAACCTCGATGTTG	1320
Db	1261	ACCTCAGCCAGGATCTGGCACTCTGGTCTTGAAACCTCGATGTTG	1320
QY	1321	TGAGGCCATGCCCTGAGACTGAGCTGAGCTGGGTGTTGATCTGAGCTCG	1380
Db	1321	TGAGGCCATGCCCTGAGACTGAGCTGAGCTGGGTGTTGATCTGAGCTCG	1380
QY	1381	GCCCCAAGCTGCGCCCTGAGACTCTCTTCTGTTGAGAAATAGGGTATT	1440
Db	1381	GCCCCAAGCTGCGCCCTGAGACTCTCTTCTGTTGAGAAATAGGGTATT	1440
QY	1441	TCTCTCTGAGAGCACTAACCCAGTGGAGAGATGGGTAGACACTGCT	1500
Db	1441	TCTCTCTGAGAGCACTAACCCAGTGGAGAGATGGGTAGACACTGCT	1500
QY	1501	TCTGGAAATTGGTAGTAGTTCTAGGCCACCCATTATGATCTGATCAGCTG	1560
Db	1501	TCTGGAAATTGGTAGTAGTTCTAGGCCACCCATTATGATCTGATCAGCTG	1560
QY	1561	GAGCAGGCGAGGATGTTGCAATGCAATTGAGATTAGTGA	1620
Db	1561	GAGCAGGCGAGGATGTTGCAATGCAATTGAGATTAGTGA	1620
QY	1621	TCCTTGCACCGTCTAGTAGTTAAATACCCATTTATGAGGGATA	1680
Db	1621	TCCTTGCACCGTCTAGTAGTTAAATACCCATTTATGAGGGATA	1680
QY	1681	GGCTCCCGAGCTTAAAGGAACTCGCTAGGTCTAACGTTAGGTAGGAGGAGGCTGGAT	1740
Db	1681	GGCTCCCGAGCTTAAAGGAACTCGCTAGGTCTAACGTTAGGTAGGAGGAGGCTGGAT	1740
QY	1741	CTGAAACCAGGGTCTAGGCCAGGGGAGCTCGTAGGTCTAACGTTAGGTAGGAGGCTGGAT	1800
Db	1741	CTGAAACCAGGGTCTAGGCCAGGGGAGCTCGTAGGTCTAACGTTAGGTAGGAGGCTGGAT	1800
QY	1801	CAGGGAGGGAGCTGAGGTCTGGGCCCCATGGAGTAAGGGAGCCCTCCGGCGG	1860
Db	1801	CAGGGAGGGAGCTGAGGTCTGGGCCCCATGGAGTAAGGGAGCCCTCCGGCGG	1860
QY	1861	ATCGAGCTGCTGAGGTCTACGTGAAAGCCCTCGAGATTAAGCGCGTGTACCGCAA	1920
Db	1861	ATCGAGCTGCTGAGGTCTACGTGAAAGCCCTCGAGATTAAGCGCGTGTACCGCAA	1920
QY	1921	AAAATAAAAATAAAA 1939	
Db	1921	AAAATAAAAATAAAA 1939	
RESULT 4			
AAA46932			
ID			
AAA46932 standard; cDNA; 1939 BP.			

PP 16-OCT-2001; 2001US-0978697.
 PR XX
 PR 07-OCT-1998; 99WO-US21141.
 PR 20-NOV-1998; 99WO-US24855.
 PR 05-JAN-1999; 99WO-US00106.
 PR 09-MAR-1999; 99WO-US0028.
 PR 10-MAR-1999; 99WO-US0190.
 PR 14-MAY-1999; 99WO-US0733.
 PR 02-TUN-1999; 99WO-US1222.
 PR 30-NOV-1999; 99WO-US24313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28555.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US09439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 01-AUG-2000; 2000WO-US2328.
 PR 01-DEC-2000; 2000WO-US2678.
 PR 28-FEB-2001; 2001WO-US00520.
 PR 22-MAR-2001; 2001WO-US0552.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US1800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 17-OCT-1997; 97US-062350P.
 PR 03-NOV-1997; 97US-062449P.
 PR 13-NOV-1997; 97US-06511P.
 PR 21-NOV-1997; 97US-066364P.
 PR 10-MAR-1998; 98US-077450P.
 PR 11-MAR-1998; 98US-077632P.
 PR 11-MAR-1998; 98US-077641P.
 PR 11-MAR-1998; 97US-077649P.
 PR 12-MAR-1998; 98US-077791P.
 PR 13-MAR-1998; 98US-078004P.
 PR 20-MAR-1998; 98US-078866P.
 PR 20-MAR-1998; 98US-078910P.
 PR 20-MAR-1998; 98US-078936P.
 PR 25-MAR-1998; 98US-07939P.
 PR 26-MAR-1998; 98US-079656P.
 PR 27-MAR-1998; 98US-079663P.
 PR 27-MAR-1998; 98US-079664P.
 PR 27-MAR-1998; 98US-079689P.
 PR 27-MAR-1998; 98US-079728P.
 PR 27-MAR-1998; 98US-079786P.
 PR 30-MAR-1998; 98US-079920P.
 PR 30-MAR-1998; 98US-079923P.
 PR 26-MAY-1998; 81US-026721.
 PR 17-MAR-1998; 98US-0040220.
 PR 26-TUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0169978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187368.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-028517.
 PR 05-MAR-1999; 99US-025465.
 PR 10-MAR-1999; 99US-0265686.

PR 12-APR-1999; 99US-0284291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 08-NOV-2000; 2000US-0709238.
 PR 27-NOV-2000; 2000US-0723749.
 PR 20-DEC-2000; 2001US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-087403.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0185585.
 PR XX
 PA (GERH) GENENTECH INC.
 PR XX
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Baton D,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Klagsbrun M, Kuo SS, Napier MA, Pan J, Paoni NP, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX DR WPI; 2003-288163/28.
 PR P-PSDB; ABU61101.

CC PT Novel secreted and transmembrane polypeptides and polynucleotides
 CC encoding them useful for treating cancer, kidney diseases, bone,
 CC cartilage disorders and immune deficiencies -
 PT
 XX
 PS Claim 2; Fig 74; 459PP; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane protein. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for for identifying agonists or antagonists. The
 CC biactive molecule maybe a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumors, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, for the genetic
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC The present sequence encodes a human PRO polypeptide of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 XX seqdata.uspto.gov/pstipidQuery.html.

SQ Sequence 1939 BP; 367 A; 549 C; 624 G; 399 T; 0 other;

Query Match 100%; Score 1939; DB 25; Length 1939;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCCTCGCTCGAGGTGACCGCCGGGGGGTCCAGGCCGCTGCAAGGGGAT 60
 Db 1 CGCTCCGCGCTTGGAGGTGACGCCGCGGGGGTCCAGGCCGCTGCAAGGGGAT 60
 QY 61 CGCGCGCCGCTTGGAGGTGACGCCGCGGGGGTCCAGGCCGCTGCAAGGGGAT 60
 Db 61 CGCGCGCCGCTTGGAGGTGACGCCGCGGGGGTCCAGGCCGCTGCAAGGGGAT 120
 QY 121 GGCGGGGATGAGGCGCTGCTGGGGGGTTGTCAGGCCGCTTACGGCTT 180

Db 121 GCGCCGCGATGGAGGCCGCTGTCTGGGGGGTGTGCTGGCTTAGTCGTTGT 180
 QY 181 CTACTACACCTGTGAGGCCGGCGCTGTGAGGCCGCTGTGAGGCCGCTGTG 240
 Db 181 CTACTACACCTGTGAGGCCGCTGTGAGGCCGCTGTGAGGCCGCTGTG 240
 QY 241 GACCGTGTCAACGGCSCAACAGCGGCATCGGAAGGTGACGGGCTGACTGAGGG 300
 Db 241 GCGCGGTCACGGCGAACAGGGCATCGGAAGGTGACGGGCTGACTGAGGG 300
 QY 301 CGGGAGGGCGCTGTGAGGTGCTGGCGCAGAGCGGGAGGGCTGTG 360
 Db 301 CGGGAGGGCGCTGTGAGGTGCTGGCGCAGAGCGGGAGGGCTGTG 360
 QY 421 TCTGGCTCGGAGGGCTTGAGGAACTATGGGTATCTCATGGCTTGAGCTGGCGA 420
 Db 421 TCTGGCTCGGAGGGCTTGAGGAACTATGGGTATCTCATGGCTTGAGCTGGCGA 420
 QY 481 CCTCATCCAACTGGCGCTATCGTCTCTGCGCGAACCGTGGCTTAACCTGTG 540
 Db 481 CCTCATCCAACTGGCGCTATCGTCTCTGCGCGAACCGTGGCTTAACCTGTG 540
 QY 541 GCTTCGGGGGACCATATGGCGCTTCTGCGACKATCTCTGCGCTTGCGA 600
 Db 541 GCTTCGGGGGACCATATGGCGCTTCTGCGACKATCTCTGCGCTTGCGA 600
 QY 601 GGATGTCGCCCCATAGCGCGCTGAGCTCGTGCCTGCTGCTG 660
 Db 601 GGATGTCGCCCCATAGCGCGCTGAGCTCGTGCCTGCTGCTG 660
 Db 661 TCACTTAAACCGCTGGACCGCCAGTGTGGCTGCGCTGCGGAGSTCGCGCATATGC 720
 Db 661 TCACTTAAACCGCTGGACCGCCAGTGTGGCTGCGCTGCGGAGSTCGCGCATATGC 720
 QY 721 TGACACTTAACTGTGCTATGACTGTGTTGGCGGACCTGGCACCGCTGAGGCC 780
 Db 721 TGACACTTAACTGTGCTATGACTGTGTTGGCGGACCTGGCACCGCTGAGGCC 780
 QY 781 TGGTCACTCTGTGCTATGACTGTGTTGGCGGACCTGGCACCGCTGAGGCC 840
 Db 781 TGGTCACTCTGTGCTATGACTGTGTTGGCGGACCTGGCACCGCTGAGGCC 840
 QY 841 TGGTCCCTGAGCTGTGGCCCACTTGGCCATTTGGCTGTGGCTGTGGCTGTGG 900
 Db 841 TGGTCCCTGAGCTGTGGCCCACTTGGCCATTTGGCTGTGGCTGTGG 900
 QY 901 AAGAGGGGGCCAGACCCCTGATTGTCTTCAAGGGCATCGAGCCCTGAG 960
 Db 901 AAGAGGGGGCCAGACCCCTGATTGTCTTCAAGGGCATCGAGCCCTGAG 960
 QY 961 TGGGAGATTTGGCCAACTGGCATGTGGAGGAGGTGCTCCAGCGACCG 1020
 Db 961 TGGGAGATTTGGCCAACTGGCATGTGGAGGAGGTGCTCCAGCGACCG 1020
 QY 1021 GCGAGCCCATCTGCTGTGGAGGAGGTGCTCCAGCGACCG 1080
 Db 1021 GCGAGCCCATCTGCTGTGGAGGAGGTGCTCCAGCGACCG 1080
 QY 1081 TGGTCACTCTGTGCTATGACTGTGTTGGCGGACCTGGCACCGCTGAGGCC 1140
 Db 1081 TGGTCACTCTGTGCTATGACTGTGTTGGCGGACCTGGCACCGCTGAGGCC 1140
 QY 1141 CCCCAACCTGGAGGCCAGTTGGCTTAACTTACCCAGCCCTGAGGTGACCGA 1200
 Db 1141 CCCCAACCTGGAGGCCAGTTGGCTTAACTTACCCAGCCCTGAGGTGACCGA 1200
 QY 1201 TTGTCTTAACTTACCCAGCCGAACTGGCTTAACTTACCCAGCCCTGAGGTGACCGA 1260
 Db 1201 TTGTCTTAACTTACCCAGCCGAACTGGCTTAACTTACCCAGCCCTGAGGTGACCGA 1260

RESULT 6
 ABL90069 ID: ABL90069 standard, cDNA, 1887 BP.
 XX AC ABL90069;
 XX DT 24-MAY-2002. (first entry)
 XX DR Human polynucleotide SEQ ID NO 631.
 XX KW Cytotoxic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antilicer;
 KW vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiotonic; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.
 OS Homo sapiens.
 XX MO20190304-A2.
 XX PD 29-NOV-2001.
 PP 18-MAY-2001; 2001W0-US16450.

QY 1031 CGCTTATGGAGCCAGCAGAGGCTGACAGGCTTGAGGAGGATGTGAAACC 1090 KW
 QY 882 CGCTTATGGAGCCAGCAGAGGCTGACAGGCTTGAGGAGGATGTGAAACC 941 KW
 Db 1091 GATGAGAGGCCAGTCAGTCAAGGACTCAAGGGCCATTTCATAACCAACCT 1150 KW
 QY 942 GATGAGAGGCCAGTCAGTCAAGGACTCAAGGGCCATTTCATAACCAACCT 1001 KW
 QY 1151 GAGGAGGCCAGTCAGTCAAGGACTCAAGGGCCATTTCATAACCAACCT 1210 KW
 Db 1002 GAGGAGGCCAGTCAGTCAACCTAACCCASCCCTAGAGCTGAGGGCCATTTCATAACCAACCT 1061 KW
 QY 1211 ATGAGGCACCGAATTCAAGGCTTAAGTTGAGCTGAGAATCAGCTCTCGGC 1270 KW
 Db 1062 ATGAGGCACCGAATTCAAGTCAAGGCTAAGTGTAGCTGAGCTGAGAATCAGCTCTCGGC 1121 KW
 QY 1271 CAGGATGCTGCAATGGCACTCATGGCTGAAATCCGAAATGTTGAGGGATG 1330 PR
 Db 1122 CAGGATGCTGCAATGGCACTCATGGCTGAAATCCGAAATGTTGAGGGATG 1181 PR
 QY 1331 CCCCTGGACCTCTGAGGGTTGTGATCTGAGCTCCCGTGTGTTACTTCGGGCCCCAAGC 1390 PA
 Db 1182 CCTGGACACTGAGGGTTGTGAGCTGGCTGAGCTCGTGTGTTACTTCGGGCCCCAAGC 1241 PA
 QY 1391 TGGGCCCTGGACATCTCTTCTGGTGAAGGATAATGGGTGATTTCCTCGG 1450 XX
 Db 1242 TGAGCCCTGGACATCTCTTCTGGTGAAGGATAATGGGTGATTTCCTCGG 1301 XX
 QY 1451 AGTGACAGTACCCAGGAGATGGAGATGGGAATGAGACTGTGGCTTCGGAAAT 1510 XX
 Db 1302 AGTGACAGTACCCAGGAGATGGAGATGGGAATGAGACTGTGGCTTCGGAAAT 1361 XX
 DR WO20027186-A2.
 QY 1511 TTGGATGTTGTTTCAAGGCCACCTTATGATCTGATGAGCTGTGGAGAGC 1570 XX
 Db 1362 TTGGATGTTGTTTCAAGGCCACCTTATGATCTGATGAGCTGTGGAGAGC 1421 XX
 QY 1571 AGGGAGTTGCAATGTGATGACTGCAACATGGAGATAATGAGATCTGATCTCGGA 1630 CC
 Db 1422 AGGGAGTTGCAATGTGATGACTGCAACATGGAGATAATGAGATCTGATCTCGGA 1481 CC
 QY 1631 ACCTCTACTGTTAGTAGTAAATTACCCATGTTAATAGGGATTAGCTCCGAG 1690 CC
 Db 1482 ACCTCTACTGTTAGTAGTAAATTACCCATGTTAATAGGGATTAGCTCCGAG 1541 CC
 QY 1691 CTAGGGACTCGCTGAGCTCAGCAGTAGTGGAGGAGGGCTGTGGATCTGACCCAA 1750 CC
 Db 1542 CTAGGGACTCGCTGAGCTCAGCAGTAGTGGAGGAGGGCTGTGGATCTGACCCAA 1601 CC
 QY 1751 GGAGTGGAGCCAGGGCACTGGCGTAGATGGTGTGAGTGTGAGGGGG 1810 XX
 Db 1602 GGGCTGAGCCAGGGCACTGGCGTAGATGGTGTGAGTGTGAGGGGG 1661 XX
 QY 1811 CAGCTGTTATGGAGTGCCTACGGACTAGGGACCTCTGGGGGAGGCT 1870 XX
 Db 1662 CAGCTGTTATGGAGTGCCTACGGACTAGGGACCTCTGGGGGAGGCT 1721 XX
 QY 1871 GGGGTCACTGTGATCTGAGGCCCTCGGGATAAAGCCTGTTGACGCC 1918 XX
 Db 1722 GGCTCTCTGTTCTGAGGCCCTCGGGATAAAGCCTGTTGACGCC 1769 XX
 RESULT 8
 ABZ68100 ID ABZ68100 standard; DNA; 1098 BP.
 AC XX
 AC ABZ68100;
 DT 26-MAR-2003 (first entry)
 XX Human secreted protein encoding genomic DNA SEQ ID NO 1623.
 KW Human; secreted protein; nootropic; neuroprotective; cytostatic;

virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV; KW
 KW vulneary; antibacterial; antiparkinsonian; antisickling; antianemic; KW
 KW antiarthritic; cancer; antirheumatic; hepatoprotective; cerebroprotective; KW
 KW antiinflammatory; antiallergic; antidiabetic; antulcer; anticonvulsant; KW
 KW antifungal; antiparasitic; cardiant; immune disorder; nephrotropic; KW
 KW cardiovascular disorder; neurological disease; gene therapy; gene; ds. KW
 KW gene therapy; gene; ds.
 Homo sapiens.
 XX
 PN WO20027186-A2.
 PD 03-OCT-2002.
 XX
 PP 26-MAR-2002; 2002WO-US09188.
 XX
 PR 27-MAR-2001; 2001US-278650P.
 PR 12-SEP-2001; 2001US-095082.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR XX
 QY XX
 PT New human secreted proteins encoded by genes contained in cDNA clones PT
 PT (e.g., HGCA19), useful for preventing, treating or diagnosing e.g. AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne PT
 PT disclosure, Page 2253-2254; 2423pp; English.
 XX
 CC The invention relates to novel human genes (ABZ6891-ABZ68209) and the CC
 encoded secreted proteins (ABP9470-ABP9872) useful for preventing, CC
 treating or ameliorating medical conditions e.g. by protein or gene CC
 therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and CC
 (ant)agonists are useful in the diagnosis, treatment and prevention of:
 (a) cancer, e.g. breast and ovarian cancer and other cancers of the CC
 adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, CC
 lung or uterine; (b) immune disorders e.g. Addison's disease, CC
 allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, CC
 diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid CC
 arthritis and ulcerative colitis; (c) cardiovascular disorders such as CC
 myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. CC
 cerebral anoxia and spinafis; and (f) infectious diseases such as viral, CC
 bacterial, fungal and parasitic infections.
 XX
 SQ Sequence 1098 BP; 243 A; 286 C; 326 G; 243 T; 0 other;
 Query Match Best Local Similarity 40.2%; Score 779; DB 25; Length 1098;
 Matches 979; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 936 TACAAAGGGCTGAGCCCTCAGTGGAGATATTGCACTGCGATGGAGG 995
 Db 113 TACAAAGGGCTGAGCCCTCAGTGGAGATATTGCACTGCGATGGAGG 172
 QY 996 TGGCTTCACTGAGCCAGGAGCCGGCGAGGCTATGGGGCCAGGAGG 1055
 Db 173 TGGCTTCACTGAGCCAGGAGCCGGCGAGGCTATGGGGCCAGGAGG 232
 QY 1056 TGGCTTCACTGAGCCAGGAGCCGGCGAGGCTATGGGGCCAGGAGG 1115
 Db 233 TGGCTTCACTGAGCCAGGAGCCGGCGAGGCTATGGGGCCAGGAGG 292
 QY 1116 CAGAGGCCCACTCTCTGAGGCCCTGGAGCTGGAGCTGGAGCTGGAGCT 1175
 Db 293 CAGAGGCCCACTCTCTGAGGCCCTGGAGCTGGAGCTGGAGCTGGAGCT 352
 QY 1176 ACCCCACCTCTGAGGTCACCTGAGCTGGAGCTGGAGCTGGAGCT 1235

Db	353	ACCCAGCCTCAGAGCTCACCGATTTGTCMAGATACACGCCACGRATCAGGTAAG	412	PR XX	11-JUN-1999; 99US-0138625.
Qy	1236	TGAGCTGAGATCCAGCTCTAACCTAACCTAGGCAGKAGTGTGCAAGCCTCAT	1295	PA XX	(HUMA-) HUMAN GENOME SCI INC.
Db	413	TTCAGCCCTGAGATCCAGCTCTAACCTAACCTAGGCAGKAGTGTGCAAGCCTCAT	472	PI XX	Rosen CA, Ruben SM, Komatsoulis GA;
Qy	1296	GTCCTTGAAACCTCGATGTTGAGGCAATGCCCTGGAGACTGAC3GTTGTAT	1355	DR XX	WPI; 2001-071148/08.
Db	473	GTCCTTGAAACCTCGATGTTGAGGCAATGCCCTGGAGACTGAC3GTTGTAT	532	PT XX	Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
Qy	1356	CITGACTTCGGTTACTTCTGGGCCAGCTGCGCTGACATCTTTCCTG	1415	PT XX	
Db	533	CTTGACCCCGTGTACTTCTGGGCCAGCTGCGCTGACATCTTTCCTG	592	PS XX	Claim 1; Page 463; 525pp; English.
Qy	1416	GTGAGGATAATGGTATTCTCTGGAGTGACGTAACCCGATGGAGA	1475	CC CC	The present invention relates to 26 secreted human proteins. The present invention relates to 26 secreted human proteins. The
Db	593	GTGAGGATAATGGTATTCTCTGGAGTGACGTAACCCGATGGAGA	652	CC CC	proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression.
Qy	1476	ATAGGGTATGTCAGACCTGCTCTGGAAATTGAGTAGTATTCTCAGGCCC	1535	CC CC	For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and any involving abnormal angiogenesis, neurodegeneration and/or infectious diseases.
Db	653	ATAGGGTATGTCAGACCTGCTCTGGAAATTGAGTAGTATTCTCAGGCCC	712	CC CC	
Qy	1536	CCCTTATGATCTGATGAGCTGCTGAGCAGAGGGCGGAGCTGATGATGACTG	1595	CC CC	
Db	713	CCCTTATGATCTGATGAGCTGCTGAGCAGAGGGCGGAGCTGATGACTG	772	CC XX	
Qy	1596	CCACATGAGATTGAACTGATGCCCTTGCAACCTCTAGCTAGGTTAAATA	1655	SQ Sequence 1140 BP; 269 A; 297 C; 330 G; 244 T; 0 other;	
Db	773	CCACATGAGATTGAACTGATGCCCTTGCAACCTCTAGCTAGGTTAAATA	832	Query Match 36.0%; Score 698; DB 22; Length 1140; Best Local Similarity 99.5%; Pred. No. 7.3e-262; Matches 1088; Conservative 0; Mismatches 3; Indels 2; Gaps 2;	
Qy	1656	CCCCATGTAAATGAAAGGGAATTGCTCCGAGCTAAGCTGGCTTAGGTCAC	1715	Qy Db	827 CTGTCCTGCCTCATTTCTGGAGCTGGCCCATGGCTGGCTGG 886
Db	833	CCCCATGTAAATGAAAGGGAATTGCTCCGAGCTAAGCTGGCTTAGGTCAC	892	Qy Db	13 CTGTCCTGCCTCATTTCTGGAGCTGGCTGGCCCATGGCTGG 72
Qy	1716	AGTGAATGAGGAGGAGCCCTGGATCTGAAACCAAGGGCTTGAGGCCAGCTGCC	1775	Qy Db	887 GTGCTGGGACCAAGAGGGGTGGAGCACCCCTGATGTCAGGGGG 946
Db	893	AGTGAATGAGGAGGAGCCCTGGATCTGAAACCAAGGGCTTGAGGCCAGCTGCC	952	Qy Db	73 GTGCTGGGACCAAGAGGGGTGGAGCACCCCTGATGTCAGGGGG 132
Qy	1776	GTAGATGGCTGAGNAGTGAGTCGGGAGGGCTGGTATGAGCTGGCCATG	1835	Qy Db	947 ATCGACCCCTCAGGGAGATTGGCAACTSCATGTTGAGGGCTTCAGGT 1006
Db	953	GTAGATGGCTGAGNAGTGAGTCGGGAGGGCTGGTATGAGCTGGCCATG	1012	Qy Db	133 ATGACCCCTCAGGGAGATTGGCAACTSCATGTTGAGGGCTTCAGGT 192
Qy	1836	GAGTAGGGAGCCTCCGGAGGGATGGAGCTGGGCTGGGTCATGAGCCCT	1895	Qy Db	1007 GCGGAGACGGCCAGGCCATGGCTATGGGGCAGGAGGGCTGGAGGCT 1066
Db	1013	GAGTAGGGAGCCTCCGGAGGGATGGAGCTGGGTCATGAGCCCT	1072	Qy Db	193 GCGGAGACGGCCAGGCCATGGGGCTGGGTCATGAGCCCT 252
Qy	1896	CGGATTAAGCGCGTGTACGCC 1918		Qy Db	1067 GGGCTGGGAGGAGCTGAGCCGATGAAACCCGAGCTGAGACTCGAGGCCA 1126
Db	1073	CGGATTAAGCGCGTGTACGCC 1095		Qy Db	253 GGGCTGGGAGGAGCTGAGCCGATGAAACCCGAGCTGAGGCCA 312
RESULT 9					
AAFP26578			Qy	1127 TCTCTCTAAGCACCCACCTGGAGGCCACGGTTCACCTTACCCACCT	1186
ID	AAFP26578	standard; DNA; 1140 BP;	Db	313 TCTCTCTAAGCACCCACCTGGAGGCCACGGTTCACCTTACCCACCT	372
XX	AAFP26578;		Qy	1187 CAGAGCTCACAGATTGTCTAGATGACGCCGAACTCGGTAAGTGAGCTGAG	1246
AC			Db	373 CAGAGCTCACAGATTGTCTAGATGACGCCGAACTCGGTAAGTGAGCTGAG	432
DT	27-MAR-2001	(first entry)	Qy	1247 AACCGCTCTAACCTAGGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAG	1306
XX			Db	433 ATCCAGCTCTAACCTAGGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAG	492
DR			Qy	1307 ACCTCGATGTTGAGGCCATGCCCTGGAGACTGAGCTGAGCTGAGCTGAG	1366
DN			Db	493 ACCTCGATGTTGAGGCCATGCCCTGGAGACTGAGCTGAGCTGAGCTGAG	551
DN			Qy	1367 TGGTACTCTGGAGGCTGGCTGGAGCTGAGCTGAGCTGAGCTGAGCTGAG	1425
PN	W020076531-A1.		Db	552 TGGTACTCTGGAGGCTGGCTGGAGCTGAGCTGAGCTGAGCTGAGCTGAG	611
XX	21-DEC-2000.		Qy	1426 TAATGGTATTCTCTGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	1485
PP	01-JUN-2000; 2000WO-US15137.				
XX					

QY	612 TAATGGGAGTATTCTCTGAGAGTAGACCACTCAGAGGAGATGGGTAT 671
PT	New human secreted proteins encoded by genes contained in cDNA clones (e.g. HCCAC19), useful for preventing, treating or diagnosing e.g.
PT	ADSD, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or West Nile fever
XX	
PS	Claim 7; Page 1350-1351; 2423pp; English.
QY	1485 GCTAGACACTGTGCTTCGGAAATTGATGTTAGTAATTCAGGCCACCTTATGA 1545
Db	732 TTCTGATCAGCTCGAGCAGAGGAGGTTGCACTGTGATGACTGCCAACATTA 731
QY	1546 TTCTGATCAGCTCGAGCAGAGGAGGTTGCACTGTGATGACTGCCAACATTA 1605
Db	732 TTCTGATCAGCTCGAGCAGAGGAGGTTGCACTGTGATGACTGCCAACATTA 791
QY	1606 GAATTTAGTAGACTGATTCCTTGACACCTCTAGTAGTAAATTACCCATTT 1665
Db	732 TTCTGATCAGCTCGAGCAGAGGAGGTTGCACTGTGATGACTGCCAACATTA 792
QY	1666 AATGAGCGGAATTTAGGCTCCGAGCTAAGGACTCGCTAGGCTCACAGTAG 1725
Db	852 AATGAGCGGAATTTAGGCTCCGAGCTAAGGACTCGCTAGGCTCACAGTAG 911
QY	1726 AGGAGGCTCTGGGATCTGAAACCAGGGCTGAGCCAGGGCCACCTGCGTAA 1785
Db	912 AGGAGGCTCTGGGATCTGAAACCAGGGCTGAGCCAGGGCCACCTGCGTAA 1786
QY	1786 TGCCTGAGAGTGTGAGCTGAGCAGGCAAGGCTGAGGCTGCCCCAGGAG 1845
Db	972 TGCCTGAGAGTGTGAGCTGAGCAGGCAAGGCTGAGGCTGCCCCAGGAG 1031
QY	1846 ACGGCTTCGGGCGATGGGGCTCATGTGATCTGAAACCCCTCGGATAAAG 1905
Db	1032 ACGGCTTCGGGCGATGGGGCTCATGTGATCTGAAACCCCTCGGATAAAG 1091
QY	1906 CGCGTGACGCC 1918
Db	1092 CGCGTGACGCC 1104
RESULT 10	
AB267229	Human secreted protein encoding cDNA SEQ ID NO 349.
ID	AB267229 standard; cDNA; 1140 BP.
XX	
AC	
XX	
DT	26-MAR-2003 (first entry)
XX	
DB	
QY	827 CTGTCCTCGGCCATGTCCTGGATGCTGCGCCACTTTGCCCATATGCTTGCTG 886
Db	887 GTGTCCTCGGCCATGTCCTGGATGCTGCGCCACTTTGCCCATATGCTTGCTG 72
QY	887 GTGTCCTCGGCCATGTCCTGGATGCTGCGCCACTTTGCCCATATGCTTGCTG 946
Db	73 GTGTCCTCGGCCATGTCCTGGATGCTGCGCCACTTTGCCCATATGCTTGCTG 132
QY	947 ATCGAGCCCTCACTGGAGATATTGCAACTGCCATGTGAGAGGTGCTTCAGCT 1006
Db	133 ATCGAGCCCTCACTGGAGATATTGCAACTGCCATGTGAGAGGTGCTTCAGCT 192
QY	1007 GCCGAGAGGAGGGGGAGCCATGGCTATGGAGGCCAGAAGAGGGTGGGGCT 1066
Db	193 GCCGAGAGGAGGGGGAGCCATGGCTATGGAGGCCAGAAGAGGGTGGGGCT 252
QY	1067 GG3CCTGGGAGGATGCTGAAACGATGAGACGCCACTCTGAGACTCAGAGGCCA 1126
Db	253 GG3CCTGGGAGGATGCTGAAACGATGAGACGCCACTCTGAGACTCAGAGGCCA 312
QY	1127 TCTCTCTAGACCCCCACCTCTAGGGGCCAGTTCTCACTTACCCAGGCT 1186
Db	313 TCTCTCTAGACCCCCACCTCTAGGGGCCAGTTCTCACTTACCCAGGCT 372
QY	1187 CAGAGCTCACCAAGATGCTAAGATGAGGCCACCGAATTCAGGTTAGTGGCTGAG 1246
OS	
XX	
PN	WO20027186-A2.
XX	
PD	03-OCT-2002.
XX	
PR	26-MAR-2002; 2002MO-US09188.
PR	27-MAR-2001; 2001US-270650P.
PR	12-SEP-2001; 2001US-090082.
PR	12-SEP-2001; 2001US-090083.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PT	Rosen CA, Ruben SM;
DR	WPI: 2003-040583/03.
PR	P-PSSB, ABP98808.
XX	

XX
 DT 09-APR-2001 (first entry)
 XX
 DB Novel human polynucleotide, SEQ ID NO: 2250.
 XX
 KW Human; cytostatic; gene therapy; colon cancer; prostate cancer;
 KW breast cancer; lung cancer; cancer detection; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2001025568-A2.
 XX
 PD 11-JAN-2001.
 XX
 PP 30-JUN-2000; 2000WO-US18374.
 XX
 PR 02-JUL-1999; 99PCT-0142310.
 XX
 PR 02-JUL-1999; 99US-0142311.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PA (HISE-) HISEQ INC.
 XX
 PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kasseam A;
 PI Reinhard C, Randazzo P, Kennedy GC, Pot D, Lamson G, Drmanac R;
 PI Crenjaku R, Drmanac S, Dickson M, Lapat I, Leibkowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Crain B;
 DR WPI, 2001-091805/10.
 XX
 PT Library of polynucleotides for diagnosing a cancerous state of a
 mammalian cell and detecting cancer, particularly of the colon or
 prostate, comprises 3351 human polynucleotide sequences -
 XX
 PS Claim 9; Page 873; 1046pp; English.

The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell and can
 CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotide and for detection of transcription levels. Ribozymes
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibodies against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia.
 XX
 SQ Sequence 397 BP; 74 A; 125 G; 82 T; 0 other;
 Query Match 10.3%; Score 200; DB 22; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.7e-68; Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 TATGTGACACTAAGCTGGTAATGTTGACTGTTGCCGAGCTGGCTGGCCACCGAGCTTGAG 775
 Db 31 TATGTGACACTAAGCTGGTAATGTTGACTGTTGCCGAGCTGGCCACCGAGCTTGAG 90
 QY 776 GGCCTGGCTCACCTGCTATGAGCCACCCAGGGCTTGAACTCGAGCTGGCTGGAGTCAG 835
 Db 91 GGCCTGGCTCACCTGCTATGAGCCACCCAGGGCTTGAACTCGAGCTGGAGTCAG 150
 QY 836 CGCATGTTCTGGATGGCTGGCCACTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 895
 Db 151 CGCCATGTTCTGGATGGCTGGCCACTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 210
 QY 896 GCACCAAGAGGGGGCCCA 915
 Db 211 GCACCAAGAGGGGGCCCA 230

RESULT 13
 XX
 AT19666 ID AT19666 standard; cDNA to mRNA; 186 BP.
 XX
 AC AT19666;
 XX
 DT 28-JUN-1996 (first entry)
 DB Human gene signature HUMGS00736.
 XX
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 OS Homo sapiens.
 XX
 PN WO9514772-A1.
 XX
 PD 01-JUN-1995.
 XX
 PR 12-NOV-1993; 93JP-0355504.
 XX
 PA (MATS-) MATSUBARA K.
 PA (OKUB-) OKUBO K.
 XX
 PI Matsubara K, Okubo K.
 DR WPI, 1995-206931/27.
 XX
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX
 PS Claim 1; Page 445; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AT196001-T26397 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

XX
 SQ Sequence 186 BP; 42 A; 42 C; 67 G; 31 T; 4 other;
 Query Match 4.7%; Score 92; DB 16; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4.1e-26; Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1744 AACCCAAGCTGAGGCCAGGGCTGGCTGGCTGGCTGGAGTCAGTCAG 1803
 Db 8 AACCCAAGCTGAGGCCAGGGCTGGCTGGCTGGCTGGAGTCAGTCAG 67

QY 1804 GGCGGGGAGCTGGTACAGGGCCATGG 1835
 Db 68 GGCGGGGAGCTGGTACAGGGCCATGG 99

RESULT 14
 XX
 ABK64203/C ID ABK64203 standard; DNA; 175 BP.

XX
 DT 09-APR-2001 (first entry)
 DB Novel human polynucleotide, SEQ ID NO: 2250.
 XX
 KW Human; cyrostatic; gene therapy; colon cancer; prostate cancer;
 KW breast cancer; lung cancer; cancer detection; ss.
 OS Homo sapiens.
 XX
 PN WO20102568-A2.
 XX
 PD 11-JAN-2001.
 XX
 PR 30-JUN-2000; 2000WO-US18374.
 XX
 PR 02-JUL-1999; 99US-0142310.
 XX
 PR 02-JUL-1999; 99US-0142311.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassan A;
 PI Reichards C, Randazzo P, Kennedy SC, Pot D, Ramson G, Drmanac R;
 PI Crkencjakov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Crain B;
 DR WPI, 2001-091805/10.
 XX
 PT Library of polynucleotides for diagnosing a dangerous state of a
 PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX
 Claim 9; Page 873; 1046pp; English.
 CC The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a dangerous state of a mammalian cell and can
 CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotides and for detection of transcription levels. Ribosomes and
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibiotics against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia.
 XX
 Sequence 397 BP; 74 A; 116 C; 125 G; 82 T; 0 other;
 Query Match 10.3%; Score 201; DB 22; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 716 TATCTGACACTAGCTGGCTAATGATCTGTGCGCCCGAGGCTCGCAACCGAGTGTAG 775
 DB 31 TATCTGACACTAGCTGGCTAATGATCTGTGCGCCCGAGGCTCGCAACCGAGTGTAG 90
 QY 776 GCACTGGGGCTGCCTGCTGATGAGGCCACCGGGCTGAACTGGGAGTCCTGGCTGCTG 835
 DB 91 GCACTGGGGCTGACTGTGATGAGGCCACCGGGCTGAACTGGCTGCTG 150
 QY 836 CSGCATGTTCTGATGCTGGCCACTTGGCCGATAGCTGGCTGGCTGGCTGGCTGGCTGG 895
 DB 151 CGGCGATGTTCTGATGCTGGCCACTTGGCCGATAGCTGGCTGGCTGGCTGGCTGGCTGG 210
 QY 896 GCCTCAGGGGGGGTGCCTA 915
 DB 211 GCCTCAGGGGGGGTGCCTA 230

RESULT 13
 AAT19666 AAT19666 Standard, cDNA to mRNA, 186 BP.
 ID AAT19666
 XX
 AC AAT19666:
 XX
 PR 28-JUN-1996 (first entry)
 XX
 DR Human gene signature HUMGS00733.
 XX
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 OS Homo sapiens.
 XX
 PN WO9514772-A1.
 XX
 PD 01-JUN-1995.
 XX
 PR 11-NOV-1994; 94WO-JP01916.
 XX
 PR 12-NOV-1993; 93JP-0355504.
 XX
 PA (MATS/) MATSUBARA K.
 XX
 PA (OKUB/) OKUBO K.
 XX
 PI Matsubara K, Okubo K;
 XX
 DR WPI; 1995-206931/27.
 XX
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX
 PS Claim 1; Page 445; 2245pp; Japanese.
 CC A single-stranded DNA (or its complementary strand or the correps.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in AAT19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues. Synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-orientated cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (e.g. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
 XX
 SQ Sequence 186 BP; 42 A; 42 C; 67 G; 31 T; 4 other;

Query Match 4.7%; Score 92; DB 16; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4.1e-26;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1744 AACCGAAGGGCTGAGGCCACGGCCACTGGCTGATGAGCTGGCTGAGAGTGAGCAG 1803
 DB 8 AACCCGAGGCTGAGGCCACGGCCACTGGCTGATGAGCTGGCTGAGAGTGAGCAG 67
 QY 1804 GGCAAGGGCACTGGCTGAGGCCACGGCCACTGGCTGATGAGCTGGCTGAGAGTGAGCAG 1835
 DB 68 GGCAGGGCTGAGGCCACGGCCACTGGCTGATGAGCTGGCTGAGAGTGAGCAG 99

RESULT 14
 ABK64203/C
 ID ABK64203 standard; DNA; 175 BP.

XX
XX ABB64203;
XX DE Human benign prostatic hyperplasia gene #98.
XX KW Homo sapiens.
XX OS WO200212440-A2.
XX PN 14-FEB-2002.
XX PR 07-AUG-2001; 2000WO-US24708.
XX PR 07-AUG-2001; 2000US-233323P.
XX PR 05-JUN-2001; 2001US-0873319.
XX (GENE-) GENS LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
XX Munger WB, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J,
XX DR WPI; 2002-257476/30.
XX PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
XX cells -
XX Disclosure; Page 109, 444pp; English.
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to prevent information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of gene given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. AB64106-ABK4660 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX Sequence 175 BP; 27 A; 62 C; 37 G; 49 T; 0 other;
Query Match 4.5%; Score 89; DB 24; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1762 CAGGGCCGACTGCGCTAAGATGGGTGCTGAGGAGTGGTCAAGGCAAGGCAGCTGGTATC 1821
Db 175 CAGGGCCGACTGCGCTAAGATGGGTGCTGAGGAGTGGTCAAGGCAAGGCAGCTGGTATC 116
Qy 1822 GAGGTGCCCATGGGAGTAAAGGAGC 1849
Db 115 GAGGTGCCCATGGGAGTAAAGGAGC 88

AA179552
ID AA179552 standard; DNA; 51 BP.
XX
XX DE Human silent SNP containing nucleic acid SEQ 6493.
XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX OS Homo sapiens.
XX PN WO20140521-A2.
XX PR 07-JUN-2001.
XX PR 30-NOV-2000; 2000WO-US32758.
XX PR 30-NOV-1999; 99US-0168138.
XX PR 29-NOV-2000; 2000US-0726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M,
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
PS Claim 1; Page 2494; 2653pp; English.
PS AA173360 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173314 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptide encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX SQ Sequence 51 BP; 6 A; 17 C; 18 G; 10 T; 0 other;
Query Match 2.6%; Score 51; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 594 GCTCTGAGGCTGTGCTCCCTGCGCTGCTGGGGTAGGCTCAGTGCCC 644
Db 1 GCTCTGAGGCTGTGCTCCCTGCGCTGCTGGGGTAGGCTCAGTGCCC 51

Search completed: January 31, 2004, 04:50:06
Job time: 557 secs